

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 12:39:38 ; Search time 44 Seconds  
(without alignments)  
478.897 Million cell updates/sec

Title: US-10-733-288A-4

Perfect score: 1140

Sequence: 1 IVGRRRAPHAMFVMSLQ.....PDAPVAFVQVNWIDSIQR 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	99.4	267	1 ELRHUL	leukocyte elastase
2	868.5	76.2	265	2 I48679	neutrophil elastase
3	637.5	55.9	256	1 PRHU3	proteinase 3 (EC 3
4	480	42.1	251	1 TRHUZ	azurocidin precurs
5	428	37.5	219	1 TRPGAZ	azurocidin - pig
6	379	33.2	266	1 ELPG	pancreatic elastas
7	366	32.1	266	1 ELRT1	pancreatic elastas
8	364	31.9	258	4 S70439	pancreatic elastasi
9	364	31.9	267	4 A56615	probable pancreati
10	344.5	30.2	261	2 S40162	cathepsin G (EC 3.
11	343.5	30.1	282	1 A13172	granzyme A (EC 3.4
12	341	29.9	258	2 I56220	trypsin 2 - rat
13	340.5	29.9	226	2 S69370	duodenase - bovine
14	338.5	29.7	255	2 A27122	cathepsin G (EC 3.
15	338.5	29.7	263	1 I55608	complement factor
16	337	29.6	244	2 A34310	mast cell proteina
17	336.5	29.5	259	1 WMS28	complement factor
18	336.5	29.5	269	2 A26823	pancreatic elastas
19	335	29.4	246	1 DBHU	complement factor
20	332.5	29.2	269	2 D26823	pancreatic elastas
21	332.5	29.2	271	1 ELRT2	pancreatic elastas
22	331.5	29.1	257	2 B45061	granzyme A (EC 3.4
23	331.5	29.1	260	2 A45061	granzyme A (EC 3.4
24	328.5	28.8	249	2 A55634	granzyme M (EC 3.4
25	327.5	28.7	271	2 A25528	pancreatic elastasi
26	326.5	28.6	265	2 T10495	chymotrypsin (EC 3
27	325	28.5	236	2 A28566	T-cell suppressor
28	325	28.5	244	2 A46721	chymase (EC 3.4.21
29	322.5	28.3	226	1 KCUF	bradyruin (EC 3.4

RESULT 1

ELRHUL

leukocyte elastase (EC 3.4.21.37) precursor [validated] - human

N;Alternate names: inflammatory serine proteinase; medullasin; neutrophil elastase  
C;Species: Homo sapiens (man)

C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 09-Jul-2004

C;Accession: A31976; S04954; S06241; A27064; S00631; A28370; A34570; A05293; A25907; S14:

R;Takahashi, H.; Nukiwa, T.; Yoshimura, K.; Quick, C.D.; States, D.J.; Holmes, M.D.; Whar

J. Biol. Chem. 263, 14739-14747, 1988

A;Title: Structure of the human neutrophil elastase gene.

A;Reference number: A31976; MUID:89008342; PMID:2902087

A;Accession: A31976

A;Molecule type: DNA

A;Residues: 1-267 <TAK>

A;Cross-references: UNIPROT:P08246; GB:M20203; GB:J04032; NID:G189147; PIDN:AAA36359.1; I

R;Farley, D.; Travis, J.; Salvesen, G.

Biol. Chem. Hoppe-Seyler 370, 737-744, 1989

A;Title: The human neutrophil elastase gene. Analysis of the nucleotide sequence reveals

A;Reference number: S04954; MUID:89374820; PMID:2775493

A;Accession: S04954

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-267 <FAR>

R;Nakamura, H.; Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.

Nucleic Acids Res. 15, 9601-9602, 1987

A;Title: Nucleotide sequence of human bone marrow serine protease (medullasin) gene.

A;Reference number: S06241; MUID:88067782; PMID:3479752

A;Accession: S06241

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-267 <NAK>

A;Cross-references: EMBL:Y00477; NID:G34529; PIDN:CAA68537.1; PID:G296665

R;Okano, K.; Aoki, Y.; Sakurai, T.; Kajitani, M.; Kanai, S.; Shimizu, T.; Shimizu, H.; Ne

J. Biochem. 102, 13-16, 1987

A;Title: Molecular cloning of complementary DNA for human medullasin: an inflammatory se

A;Reference number: A27064; MUID:88032918; PMID:2822677

A;Accession: A27064

A;Molecule type: mRNA

A;Residues: 30-267 <OKA>

A;Cross-references: EMBL:X05875; NID:G34532; PIDN:CAA29300.1; PID:G1335212

A;Note: part of this sequence, including the amino end of the mature protein, was confir

R;Farley, D.; Salvesen, G.; Travis, J.

Biol. Chem. Hoppe-Seyler 369(Suppl.), 3-7, 1988

A;Title: Molecular cloning of human neutrophil elastase.

A;Reference number: S00631; MUID:89076526; PMID:2462434

A;Accession: S00631

A;Molecule type: mRNA

A;Residues: 123-267 <FA2>

A;Cross-references: GB:M27783; NID:G182055; PIDN:AAA35792.1; PID:G182056

A;Note: the authors translated the codon TTC for residue 218 as Pro

R;Takahashi, H.; Nukiwa, T.; Bassett, P.; Crystal, R.G.

J. Biol. Chem. 263, 2543-2547, 1988

A;Title: Myelomonocytic cell lineage expression of the neutrophil elastase gene.

A;Reference number: A28370; MUID:98115408; PMID:3422232  
A;Accession: A28370  
A;Molecule type: mRNA  
A;Residues: 75-267 <TA2>  
A;Cross-references: GB:J03545; NID:gl82050; PIDN:AAA52378.1; PID:gl82051  
R;Okano, K.; Aoki, Y.; Shinizu, H.; Naruto, M. 1990  
Biochem. Biophys. Res. Commun. 167, 1326-1332, 1990  
A;Title: Functional expression of human leukocyte elastase (HLE)/medullasin in eukaryotic cells.  
A;Reference number: A34570; MUID:90211319; PMID:2322278  
A;Accession: A34570  
A;Molecule type: mRNA  
A;Residues: 1-267 <OK2>  
A;Cross-references: GB:M34379; NID:gl87116; PIDN:AAA36173.1; PID:9307123  
R;Travis, J.; Giles, P.J.; Porcellini, L.; Reilly, C.F.; Baugh, R.; Powers, J. 1980  
In Protein Degradation in Health and Disease, Ciba Foundation Symposium 75, 51-68, 1980  
A;Reference number: A94428  
A;Accession: A05293  
A;Molecule type: protein  
A;Residues: 30-66, 'G', 68-73, 'D', 75, 78-82, 'E', 84-89, 'T', 91-94, 'P', 97-100, 'L', 102-103 <TR>  
A;Experimental source: neutrophil granulocytes  
R;Sinha, S.; Watorek, W.; Karr, S.; Giles, J.; Bode, W.; Travis, J. 1987  
Proc. Natl. Acad. Sci. U.S.A. 84, 2228-2232, 1987  
A;Title: Primary structure of human neutrophil elastase.  
A;Reference number: A25907; MUID:87175647; PMID:3550808  
A;Accession: A25907  
A;Molecule type: protein  
A;Residues: 30-247 <SIN>  
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having 107-Asp  
R;Green, B.G.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagmann, W.; Lark, M.; Ma  
Arch. Biochem. Biophys. 286, 284-292, 1991  
A;Title: PMN elastases: a comparison of the specificity of human isozymes and the enzyme  
A;Reference number: S14736; MUID:91378304; PMID:1897955  
A;Accession: S14736  
A;Molecule type: protein  
A;Residues: 30-50 <GRE>  
A;Comment: This is a lysosomal proteinase found in the azurophil granules of neutrophils  
C;Comment: This elastase cleaves preferentially bonds after Ala and Val. It is believed  
C;Genetics:  
A;Gene: GDB:ELA2  
A;Cross-references: GDB:118792; OMIM:130130  
A;Map position: 19p13.3-19p13.3  
A;Introns: 23/1; 75/2; 122/3; 199/3  
A;Superfamily: trypsin; trypsin homology  
C;Keywords: emphysema; glycoprotein; hydrolase; leukocyte; lysosome; rheumatoid arthritis  
F;1-27/Domain: signal sequence #status predicted <SIG>  
F;28-29/Domain: propeptide #status predicted <PRO>  
F;30-247/Product: leukocyte elastase #status experimental <MAT>  
F;30-242/Domain: trypsin homology <TRY>  
F;248-267/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;55-71,151-208,181-187,198-223/Diulfide bonds: #status experimental  
F;70,117,202/Active site: His, Asp, Ser #status predicted  
F;88/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;124,173/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 99.4%; Score 1133; DB 1; Length 267;  
Best Local Similarity 99.5%; Pred. No. 5.6e-97;  
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGGRRAPHPFVMSIQLRGHFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60  
DB 30 IVGGRRAPHPFVMSIQLRGHFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 89  
QY 61 SRREPTROVFAVQRIFFENGTDVNLNDIVILQNGSATINANVQVLAQAGRRLLNGV 120  
DB 90 SRREPTROVFAVQRIFFENGTDVNLNDIVILQNGSATINANVQVLAQAGRRLLNGV 149  
QY 121 QCLAMGWLLGNRGIASVLOELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 180  
DB 150 QCLAMGWLLGNRGIASVLOELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 209  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNVWIDSIIR 219

Db 210 GLIHGIASFVRGCGASGLYPDAFAPVAQFVNVWIDSIIR 248

## RESULT 2

I48679  
neutrophil elastase - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
A;Accession: I48679  
R;Nuchprayoon, I.; Meyers, S.; Scott, L.M.; Suzow, J.; Hiebert, S.; Friedman, A.D. 1994  
Mol. Cell. Biol. 14, 5558-5568, 1994  
A;Title: PEBP2/CBF, the murine homolog of the human myeloid AML1 and PEBP2 beta/CBF beta 1s.  
A;Reference number: I48679; MUID:94309676; PMID:8035830  
A;Accession: I48679  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-265 <RES>  
A;Cross-references: UNIPROT:Q61515; EMBL:U04962; NID:9452556; PIDN:AAB60670.1; PID:9452556  
C;Genetics:  
A;Introns: 22/1; 74/2; 121/3; 199/3  
C;Superfamily: trypsin; trypsin homology  
F;249-242/Domain: trypsin homology <TRY>  
Query Match 76.2%; Score 868.5; DB 2; Length 265;  
Best Local Similarity 75.9%; Pred. No. 1.4e-72;  
Matches 167; Conservative 19; Mismatches 33; Indels 1; Gaps 1;  
QY 1 IVGGRRAPHPFVMSIQLRGHFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60  
DB 29 IVGGRRAPHPFVMSIQLRGHFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 88  
QY 61 SRREPTROVFAVQRIFFENGTDVNLNDIVILQNGSATINANVQVLAQAGRRLLNGV 120  
DB 89 RQERTRTQTSVQGIFFENGTDVNLNDIVILQNGSATINANVQVLAQAGRRLLNGV 148  
QY 121 QCLAMGWLLGNRGIASVLOELNVTVTSLC-RESNVCTLVGRQAGVCFDGSGLVCN 179  
DB 149 PCLAMGWGLGNRGISVLOELNVTVTSLCPRRVNVCTLVPRRQAGVCFDGSGLVCN 208  
QY 180 NGLIHGIASFVRGCGASGLYPDAFAPVAQFVNVWIDSIIR 219  
DB 209 NNLVQGISFIRGCGSGLYPDAFAPVGEFVDWINSIIR 248  
RESULT 3  
PRH3  
proteinase 3 (EC 3.4.21.-) precursor [validated] - human  
N;Alternate names: AGP7; C-ANCA antigen; neutrophil proteinase 4; p29; Wegener's granuloma  
N;Contains: myeloblastin  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A45080; B46268; A43983; JH0331; A33751; S11091; A61176; A60148; A43982; A43;  
R;Sturrock, A.B.; Franklin, K.F.; Rao, G.; Marshall, B.C.; Rebentisch, M.B.; Lemons, R.S. 1992  
J. Biol. Chem. 267, 21193-21199, 1992  
A;Title: Structure, chromosomal assignment, and expression of the gene for proteinase-3.  
A;Reference number: A45080; MUID:93016043; PMID:1400430  
A;Accession: A45080  
A;Molecule type: DNA  
A;Residues: 1-254, 'P', <STU>  
A;Cross-references: UNIPROT:P24158; GB:M97911  
R;Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E. 1992  
Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992  
A;Title: Three human elastase-like genes coordinately expressed in the myelomonocyte line  
A;Reference number: A46268; MUID:92390417; PMID:1518849  
A;Accession: B46268  
A;Molecule type: DNA  
A;Residues: 1-118, 'V', 120-134, 'AT', 137-256 <ZIM>  
A;Note: sequence extracted from NCBI backbone (NCBIN:112898, NCBIN:112900, NCBIN:112902,  
R;Labbaye, C.; Musette, P.; Cayre, Y.E. 1991  
Proc. Natl. Acad. Sci. U.S.A. 88, 9253-9256, 1991  
A;Title: Wegener autoantigen and myeloblastin are encoded by a single mRNA.

A;Reference number: A43983; MUID:92021028; PMID:1681549  
A;Accession: A43983  
A;Molecule type: mRNA  
A;Residues: 1-69,'P',71-256 <LA2>  
A;Cross-references: GB:M75154; NID:g187398; PIDN:AAA59558.1; PID:g187399  
R;Campanelli, D.; Melchior, M.; Fu, Y.; Nakata, M.; Shuman, H.; Nathan, C.; Gabay, J.E.  
J. Exp. Med. 172, 1709-1715, 1990  
A;Title: Cloning of cDNA for proteinase 3: a serine protease, antibiotic, and autoantigen  
A;Reference number: JH0331; MUID:91079774; PMID:2258701  
A;Accession: JH0331  
A;Molecule type: mRNA  
A;Residues: 'R',3-118,'V',120-134,'AT',137-254,'P' <CAM>  
A;Cross-references: GB:X55688; NID:g35687; PIDN:CAA39203.1; PID:g1335280  
A;Note: Part of this sequence, including the amino end of the mature protein, was confirmed  
R;Bories, D.; Raynal, M.C.; Solomon, D.H.; Darzykiewicz, Z.; Cayre, Y.E.  
Cell 59, 959-968, 1989  
A;Title: Down-regulation of a serine protease, myeloblastin, causes growth arrest and differentiation  
A;Reference number: A33751; MUID:90090622; PMID:2598267  
A;Accession: A33751  
A;Molecule type: mRNA  
A;Residues: 42-256 <BOR>  
A;Cross-references: GB:M29142; NID:g188983; PIDN:AAA36342.1; PID:g188984  
A;Note: The authors translated the codon GGG for residue 49 as Glu, GGC for residue 52 as  
R;Jenne, D.E.; Tschopp, J.; Luedemann, J.; Utecht, B.; Gross, W.L.  
Nature 346, 520, 1990  
A;Title: Wegener's autoantigen decoded.  
A;Reference number: S11091; MUID:90332035; PMID:2377228  
A;Accession: S11091  
A;Molecule type: mRNA  
A;Residues: 20-56 <JEN>  
R;Musette, P.; Labbaye, C.; Dorner, M.H.; Cayre, Y.E.; Casanova, J.L.; Kourilsky, P.  
Blood 77, 1398-1399, 1991  
A;Title: Wegener's autoantigen and leukemia.  
A;Reference number: A61176; MUID:91159650; PMID:2001463  
A;Accession: A61176  
A;Molecule type: mRNA  
A;Residues: 1-42 <MUS>  
R;Cross-references: EMBL:X56606; NID:g35189; PIDN:CAA39943.1; PID:g35190  
R;Goldschmeding, R.; Dolman, K.M.; Van Den Ende, M.E.; Van Der Meer-Gerritsen, C.H.; Sor  
APMIS Suppl. 19, 26-27, 1990  
A;Title: The relation of 29 kD C-ANCA antigen to proteinase 3.  
A;Reference number: A60148; MUID:91136884; PMID:2285532  
A;Accession: A60148  
A;Molecule type: protein  
A;Residues: 28-48 <COL>  
R;Rao, N.V.; Wehner, N.G.; Marshall, B.C.; Gray, W.R.; Gray, B.H.; Hoidal, J.R.  
J. Biol. Chem. 266, 9540-9548, 1991  
A;Title: Characterization of proteinase-3 (PR-3), a neutrophil serine proteinase. Struct  
A;Reference number: A43982; MUID:91236723; PMID:2033050  
A;Accession: A43982  
A;Molecule type: protein  
A;Residues: 28-61,'X',63,'D',65-67;228-244 <RAO>  
R;Wilde, C.G.; Snable, J.L.; Griffith, J.E.; Scott, R.W.  
J. Biol. Chem. 265, 2038-2041, 1990  
A;Title: Characterization of two azurophil granule proteases with active-site homology b  
A;Reference number: A43981; MUID:90130450; PMID:2404977  
A;Accession: A43981  
A;Molecule type: protein  
A;Residues: 28-45,'E',47;196-208,'X',210-215,'X',217-219 <WIL>  
R;Gabay, J.E.; Scott, R.W.; Campanelli, D.; Griffith, J.; Wilde, C.; Marra, M.N.; Seeger  
Proc. Natl. Acad. Sci. U.S.A. 86, 5610-5614, 1989  
A;Title: Antibiotic proteins of human polymorphonuclear leukocytes.  
A;Reference number: A33913; MUID:89315847; PMID:2501794  
A;Accession: C33913  
A;Molecule type: protein  
A;Residues: 28-45,'E',47 <GAB>  
R;Niles, J.L.; McCluskey, R.T.; Ahmad, M.F.; Arnaout, M.A.  
Blood 74, 1888-1893, 1989  
A;Title: Wegener's granulomatosis autoantigen is a novel neutrophil serine proteinase.  
A;Reference number: A60481; MUID:90028708; PMID:2679910  
A;Accession: A60481  
A;Molecule type: protein  
A;Residues: 28-36,'X',40-47 <NI2>

R;Ohlsson, K.; Linder, C.; Rosengren, M.  
Biol. Chem. Hoppe-Seyler 371, 549-555, 1990  
A;Title: Monoclonal antibodies specific for neutrophil proteinase 4. Production and use i  
A;Reference number: S10605; MUID:91025622; PMID:2121162  
A;Accession: S10605  
A;Molecule type: protein  
A;Residues: 28-52 <OHL>  
R;Luedemann, J.; Utecht, B.; Gross, W.L.  
J. Exp. Med. 171, 357-362, 1990  
A;Title: Anti-neutrophil cytoplasm antibodies in Wegener's granulomatosis recognize an el  
A;Reference number: PL0230; MUID:90111630; PMID:1688612  
A;Accession: PL0230  
A;Molecule type: protein  
A;Residues: 28-37,'I',39-40,'I',41-43 <LUJE>  
C;Comment: This polymorphonuclear leukocyte serine protease from azurophilic granules des  
C;Genetics:  
A;Gene: GDB:PRTN3  
A;Cross-references: GDB:126876; OMIM:177020  
A;Map position: 19p13.3-19p13.3  
A;Introns: 21/1; 76/2; 123/3; 200/3  
C;Superfamily: trypsin; trypsin homology  
C;Keywords: glycoprotein; hydrolase; polymorphonuclear leukocyte; serine proteinase  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-27/Domain: propeptide #status predicted <PRO>  
F;28-356/Product: proteinase 3 #status experimental <MAT>  
F;28-243/Domain: trypsin homology <TRY>  
F;56-72;152-209;182-188;199-224/Disulfide bonds: #status predicted  
F;71;118;203/Active site: His, Asp, Ser #status predicted  
F;129;174/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 55.9%; Score 637.5; DB 1; Length 256;  
Best Local Similarity 54.5%; Pred. NO. 2.6e-51;  
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;  
QY 1 IVGRRARPHAMPFVMSLOLR---GGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGA 57  
Db 28 IVGGEAHPHSRPMYMASLQMRGNPGSHFCGGTILHPSFVLTAACHURDIPQRULNVVVLGA 87  
QY 58 HNLSRREPTRQVFAVQIFENGTDPNVLLNDIVILQNGSATINANVQVLAQAQRRRLG 117  
Db 88 HNVRTQEPFQHFSAQVFLNNYDAENKLDILLIQLSSPANLSASVTSVQLPQQQPVP 147  
QY 118 NGVQCLAMGWLGNRGIASVQLSELNVTVVTSLCRRSNVCTLVGRQAGVCFGDSGSPL 177  
Db 148 HGTCQLAMGWRGVGADPPAQVLQELNVTVVTFPCRPHNICTFVPRKAGICFGDSGGPL 207  
QY 178 VCNGLIHGTAIFVRCGASGLYPDAPAPVAQFVNWIDSIQR 219  
Db 208 ICDGIIGQIDSFVIMGCATRLFPDFTRVALYVDWIRSLTR 249  
RESULT 4  
TRHUAZ  
azurocidin precursor [validated] - human  
N;Alternate names: cationic antimicrobial protein CAP37; heparin-binding protein; neutrofi  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1992 #sequence revision 30-Sep-1993 #text change 09-Jul-2004  
A;Accession: A46268; A46455; S16450; S18851; S15445; S14738; B33913; A60708; B43  
R;Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992  
A;Title: Three human elastase-like genes coordinately expressed in the myelomonocyte line  
A;Reference number: A46268; MUID:92390417; PMID:1518849  
A;Accession: A46268  
A;Molecule type: DNA  
A;Residues: 1-251 <ZIM>  
A;Cross-references: UNIPROT:P20160; GB:M96326; NID:g179301; PIDN:AAB59353.1; PID:g179302  
A;Note: sequence extracted from NCBI backbone (NCBIN:112883, NCBIN:112891, NCBIN:112893,  
R;Morgan, J.G.; Sukienicki, T.; Pereira, H.A.; Spitznagel, J.K.; Guerra, M.E.; Larrick,  
J. Immunol. 147, 3210-3214, 1991  
A;Title: Cloning of the cDNA for the serine protease homolog CAP37/azurocidin, a microbic  
A;Reference number: A46455; MUID:92013155; PMID:1919011  
A;Accession: A46455  
A;Molecule type: mRNA

Mon Apr 18 13:05:50 2005

A;Residues: 1-251 <NOR>  
A;Cross-references: GB:M96326; NID:9179301; PTDN:AA59353.1.; PID:g179302  
A;Note: sequence extracted from NCBI backbone (NCBIN:60386, NCBI:P60395)  
R;Almeida, R.P.; Melchior, M.; Campanelli, D.; Nathan, C.; Gabay, J.E.  
Biochem. Biophys. Res. Commun. 177, 688-695, 1991  
A;Title: Complementary DNA sequence of human neutrophil azurocidin, an antibiotic with e  
A;Reference number: S16450; MUID:91264832; PMID:2049091  
A;Accession: S16450  
A;Molecule type: mRNA  
A;Residues: 3-251 <ALM>  
A;Cross-references: EMBL:X58794; NID:g28976; PTDN:CAA41601.1; PID:g28977  
A;Accession: S18520  
A;Molecule type: protein  
A;Residues: 47-51, 'S', '53-59, 'T', '61-62, 'V', '64-87 <AL2>  
R;Pohl, J.; Pereira, H.A.; Martin, N.M.; Spitznagel, J.K.  
FEBS Lett. 272, 200-204, 1990  
A;Title: Amino acid sequence of CAP37, a human neutrophil granule-derived antibacterial  
A;Reference number: S12881; MUID:91032128; PMID:2226832  
A;Accession: S12881  
A;Molecule type: protein  
A;Residues: 27-248 <POH>  
R;Flodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wollme  
Eur. J. Biochem. 197, 535-547, 1991  
A;Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of porci  
A;Reference number: S15393; MUID:91224149; PMID:2026172  
A;Accession: S15445  
A;Molecule type: protein  
A;Residues: 27-129, 'N', '131-247 <FLO>  
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 6 in having 190-Ile  
R;Green, B.G.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagnmann, W.; Lark, M.; Ma  
Arch. Biochem. Biophys. 286, 284-292, 1991  
A;Title: PMN elastases: a comparison of the specificity of human isozymes and the enzyme  
A;Reference number: S14736; MUID:91378304; PMID:1897955  
A;Accession: S14738  
A;Molecule type: protein  
A;Residues: 27-47 <GRE>  
R;Gabay, J.E.; Scott, R.W.; Campanelli, D.; Griffith, J.; Wilde, C.; Marra, M.N.; Seeger  
Proc. Natl. Acad. Sci. U.S.A. 86, 5610-5614, 1989  
A;Title: Antibiotic proteins of human polymorphonuclear leukocytes.  
A;Reference number: A33913; MUID:89315847; PMID:2501794  
A;Accession: B33913  
A;Molecule type: protein  
A;Residues: 27-46 <GAB>  
R;Pereira, H.A.; Shafer, W.M.; Pohl, J.; Martin, L.E.; Spitznagel, J.K.  
J. Clin. Invest. 85, 1468-1476, 1990  
A;Title: CAP37, a human neutrophil-derived chemotactic factor with monocyte specific act  
A;Reference number: A60708; MUID:90237224; PMID:2332502  
A;Accession: A60708  
A;Molecule type: protein  
A;Residues: 27-68 <PER>  
R;Wasiluk, K.R.; Skubitz, K.M.; Gray, B.H.  
Infect. Immun. 59, 4193-4200, 1991  
A;Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar  
A;Reference number: A43600; MUID:92040097; PMID:1937776  
A;Accession: B43600  
A;Molecule type: protein  
A;Residues: 27-48 <WAS>  
R;Miyasaki, K.T.; Bodeau, A.L., 1992  
Infect. Immun. 60, 4973-4975, 1992  
A;Title: Human neutrophil azurocidin synergizes with leukocyte elastase and cathepsin G  
A;Reference number: A49211; MUID:93014226; PMID:1399008  
A;Accession: A49211  
A;Molecule type: protein  
A;Residues: 27-46 <MIY>  
A;Note: sequence extracted from NCBI backbone (NCBI:P116551)  
R;Shellard, J.E.; Leitch, H.A.; Logan, P.M.; McMaster, W.R.; Levy, J.G.  
Exp. Hematol. 19, 136-142, 1991  
A;Title: Purification of an in vitro inhibitor of normal myelopoiesis using a monoclonal  
A;Reference number: A61502; MUID:91122218; PMID:1991495  
A;Accession: A61502  
A;Molecule type: protein  
A;Residues: 27-48 <SHE>

R;Wilde, C.G.; Snable, J.L.; Griffith, J.E.; Scott, R.W.  
J. Biol. Chem. 265, 2038-2041, 1990  
A;Title: Characterization of two azurophil granule proteases with active-site homology to  
A;Reference number: A43981; MUID:90130450; PMID:2404977  
A;Accession: B43981  
A;Molecule type: protein  
A;Residues: 27-35, 'H', '37-46;194-217 <WIL>  
R;Pereira, H.A.; Spitznagel, J.K.; Pohl, J.; Wilson, D.E.; Morgan, J.; Palings, I.; Larri  
Life Sci. 46, 189-196, 1990  
A;Title: CAP 37, a 37 kD human neutrophil granule cationic protein shares homology with i  
A;Reference number: PH0081; MUID:90157837; PMID:2406527  
A;Accession: PH0081  
A;Molecule type: protein  
A;Residues: 27-67 <PE2>  
A;Experimental source: polymorphonuclear leukocyte  
C;Comment: This protein is homologous to serine proteinases but lacks proteolytic activit  
icrobial activity against a number of gram-negative bacteria.  
C;Genetics:  
A;Gene: GDB:AZU1  
A;Cross-references: GDB:135033; OMIM:162815  
A;Map position: 19p13.3-19p13.3  
A;Introns: 20/1; 72/2; 150/3; 198/3  
C;Superfamily: trypsin; trypsin homology  
C;Keywords: glycoprotein; inflammation  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-248/Domain: amino-terminal propeptide #status predicted <PRO>  
F;27-239/Domain: azurocidin #status experimental <MAT>  
F;67,115,203/Region: defective catalytic triad  
F;249-251/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;52-68/Disulfide bonds: #status experimental  
F;126,140,171/Binding site: carboxylate (Asn) (covalent) #status experimental  
F;149-207,180-186,197-222/Disulfide bonds: #status predicted  
Query Match 42.1%; Score 480; DB 1; Length 251;  
Best Local Similarity 45.2%; Pred. No. 8.6e-37;  
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;  
QY 1 IVGGRARPHAWPFMVSVQLRGHFCGATLIAPFVMSAAHCVANVVRVVGAAHNL 60  
DB 27 IVGGRKARPRQFPFLASIQNGRHFCCGALIHAREFVMTAASCFSQNFQSVTVLIGAYDL 86  
QY 61 SRRE-PTQVFAVQRIFFENGTDPVNLLDIVLIQLNGSATINANVOAQLPAQGRRLNG 119  
DB 87 RRRERQSRQTSISSNSSENGYDPOQLNDMLQLDREANLTSSVTIPLPLQNAIVEAG 146  
QY 120 VOCLAMGWLGRNRGIAVLOELNVTVV-TSLCRSNVCTIVRGQAGVCFDGSGLV 178  
DB 147 TRCQVAGWSQSRGSLRFRFVNVTVTPDQCRPNVCTGLTRRGICNGDGTPLV 206  
QY 179 CNGLIHGIASFVRGGCAGLYPDAPAPVAQFVNWIDSII 217  
DB 207 CEGLAHGVAFSILGPCRG--PDFFTRVALFRDWIDGVL 243  
RESULT 5  
TRPGAZ  
N;Alternate names: heparin-binding protein  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: S15393  
R;Flodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wollme  
Eur. J. Biochem. 197, 535-547, 1991  
A;Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of porci  
A;Reference number: S15393; MUID:91224149; PMID:2026172  
A;Accession: S15393  
A;Molecule type: protein  
A;Residues: 1-219 <FLO>  
A;Cross-references: UNIPROT:P80015  
R;Sorensen, H.H.; Thomsen, J.; Bayne, S.; Hojrup, P.; Roepstorff, P.  
Biomed. Environ. Mass Spectrom. 19, 713-720, 1990

[illegible]

```
RESULT 8
S70439
pancreatic elastase I (allele HEL1-16) probable splice form I - human
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 28-Apr-2003
C:Accession: S70439
R:Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
DNA Seq. 2, 303-312, 1992
A:Title: Genomic organization of the human homologue of the rat pancreatic elastase I
A:Reference number: A56615; MUID:92338395; PMID:1633328
A:Accession: S70439
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-258 <KAW>
A:Note: it is not known whether the gene is expressed
F:19-251/Domain: trypsin homology <TRY>

Query Match 31.9%; Score 364; DB 4; Length 258;
Best Local Similarity 38.3%; Pred. No. 4.4e-26;
Matches 92; Conservative 37; Mismatches 85; Indels 26; Gaps 9;

Qy 1 IVGGRRARPHAWPFMVSLQLRGG----HFCGATLIAPNFVMSAAHCVANVAVRVVLG 56
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
19 VVGGTAGRNWSPQISLQYRSGSGSWYHTCGGTLIRQNVWMTAAHCVD--YQKTRFWAG 76
Qy 57 AHNLSRREPTROVFAVORIFEN---GTDPNVLLNDIVILQNGSATINANVOVQALPAQG 113
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
77 DHNLSQNDGTEQYVSVQKIVVHPYWNDSNVAAGYDIALRLAQSVTLNSVQLGVLPQEG 136
Qy 114 RRLNGVQCLAMGWGLLGRNRIASVLQELNV--TVVTSLCRRSN-----VCTLVR 162
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
137 AILANNSPCYITGWKTKTNGQLAQTLOQAYLPSVDYAIICSSSSYWGSTVKTMTVCAGGD 196
Qy 163 GRQAGVCFDGSGLPVC--NG--LIHGIAFVRG--GCASGLYDPAPVAQFVNWIDSII 217
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
197 GVRSG-CQGDGGGLHCLVNGKYSLHGVTFSVSRGCVNSRKPTVFTFRVSAYISWINNVI 255

RESULT 9
A56615
probable pancreatic elastase (EC 3.4.21.36) pseudogene - human
N:Alternate names: pancreatic elastase I homolog; pancreatic elastase I allele HEL1-16,
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1995 #sequence_revision 17-Aug-1995 #text_change 14-Aug-1998
C:Accession: A56615; S70440
R:Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
DNA Seq. 2, 303-312, 1992
A:Title: Genomic organization of the human homologue of the rat pancreatic elastase I
A:Reference number: A56615; MUID:92338395; PMID:1633328
A:Accession: A56615
A:Molecule type: DNA
A:Residues: 1-267 <KAW>
A:Cross-references: EMBL:X62259; NID:g31246; EMBL:X62258; GB:S40923; NID:g31247; EMBL:X6
5; GB:S40856; NID:g31251; EMBL:X62256; GB:S40857; NID:g31252; EMBL:X62257; GB:S40859; NI
A:Note: sequence extracted from NCBI backbone (NCBIN:109315, NCBIN:109317, NCBIN:109319,
C:Comment: This apparently silent human homolog of pancreatic elastase I is a single-co
functional protein in some other tissue.
C:Genetics:
A:Map position: 12
C:Keywords: hydrolase; pseudogene; serine proteinase

Query Match 31.9%; Score 364; DB 4; Length 267;
Best Local Similarity 38.3%; Pred. No. 4.6e-26;
Matches 92; Conservative 37; Mismatches 85; Indels 26; Gaps 9;

Qy 1 IVGGRRARPHAWPFMVSLQLRGG----HFCGATLIAPNFVMSAAHCVANVAVRVVLG 56
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
28 VVGGTAGRNWSPQISLQYRSGSGSWYHTCGGTLIRQNVWMTAAHCVD--YQKTRFWAG 85
Qy 57 AHNLSRREPTROVFAVORIFEN---GTDPNVLLNDIVILQNGSATINANVOVQALPAQG 113
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
86 DHNLSQNDGTEQYVSVQKIVVHPYWNDSNVAAGYDIALRLAQSVTLNSVQLGVLPQEG 145
```

```
Qy 114 RRLNGVQCLAMGWGLLGRNRIASVLQELNV--TVVTSLCRRSN-----VCTLVR 162
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
146 AILANNSPCYITGWKTKTNGQLAQTLOQAYLPSVDYAIICSSSSYWGSTVKTMTVCAGGD 205
Qy 163 GRQAGVCFDGSGLPVC--NG--LIHGIAFVRG--GCASGLYDPAPVAQFVNWIDSII 217
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
206 GVRSG-CQGDGGGLHCLVNGKYSLHGVTFSVSRGCVNSRKPTVFTFRVSAYISWINNVI 264

RESULT 10
S40162
cathepsin G (EC 3.4.21.20) precursor - mouse
N:Alternate names: vimentin-specific proteinase
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S40162; A48932; S23170
R:Kulmburg, P.; Baumruker, T.
A:Title: Molecular cloning, chromosomal location, and tissue-specific expression of the n
A:Reference number: A48932; MUID:93200524; PMID:8453108
A:Accession: A48932
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <KUL>
A:Cross-references: UNIPROT:P28293; EMBL:X70057; NID:g437879; PIDN:CAA49661.1; PID:g43788;
R:Heusel, J.W.; Scarpati, E.M.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Shapiro, S.;
Blood 81, 1614-1623, 1993
A:Title: Molecular cloning, chromosomal location, and tissue-specific expression of the n
A:Reference number: A48932; MUID:93200524; PMID:8453108
A:Accession: A48932
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-261 <HEU>
A:Cross-references: GB:M96801; NID:g192383; PIDN:AAA37376.1; PID:g192384
A:Note: sequence extracted from NCBI backbone (NCBIN:127495, NCBI:P:127496)
R:Nakamura, N.; Tsuru, A.; Hirayoshi, K.; Nagata, K.
Eur. J. Biochem. 205, 947-954, 1992
A:Title: Purification and characterization of a vimentin-specific protease in mouse myelc
A:Reference number: S23170; MUID:92249339; PMID:1577012
A:Accession: S23170
A:Status: preliminary
A:Molecule type: protein
A:Residues: 21-23, X', 25-44, 'X', 46, 'X', 48, 'XXS', 52-54, 'XG', 57-59, 'P' <NAK>
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:21-238/Domain: trypsin homology <TRY>
F:64,108,201/Active site: His, Asp, Ser #status predicted

Query Match 30.2%; Score 344.5; DB 2; Length 261;
Best Local Similarity 34.1%; Pred. No. 2.8e-24;
Matches 79; Conservative 47; Mismatches 85; Indels 21; Gaps 7;

Qy 1 IVGGRRARPHAWPFMVSLQLR--GGHFCGATLIAPNFVMSAAHCVANVAVRVVLGA 57
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
21 IIGGRRARPHSPYMAFLIQSGELVDRDFVLTAAHCLGS---SINTVTLGA 76
Qy 58 HNLRSRREPTROVFAVORIFEN--GTDPNVLLNDIVILQNGSATINANVOVQALPAQGRLL 116
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
77 HNTQMRERTQQLITVLRATHRPDYNFQNIIRNDMLQLRRRRARRSGSVFVLPQASKKL 136
Qy 117 GNGVQCLAMGWGLLGRNRIASVLQELNVTV--VTSLC-----RRSNVCTLVRGRQAG 167
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
137 QPGLDLCTVAGKRVQSQRG--TNVLQEVQLRVQMDQCANRFQFYNSTQICVGNPREKS 195
Qy 168 VCFDGSGLPVCNGLIHGIAFVRGCGASGLYDPAPVAQFVNWIDSIIOR 219
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
196 AFRGDSGGPLVCNSVAQGIYSY---GSNNNGPPAVFTKIQSFPMPWKRTMRR 244

RESULT 11
A31372
granzyme A (EC 3.4.21.78) precursor [validated] - human
```



N;Alternate names: cytotoxic T-lymphocyte proteinase; cytotoxic T-lymphocyte tryptase; C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1990 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: A31372; A30525; A30526; A28943  
R:Gerstenfeld, H.K.; Hersenberger, R.J.; Shows, T.B.; Weissman, I.L.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1184-1188, 1988  
A:Title: Cloning and chromosomal assignment of a human cDNA encoding a T cell- and natural killer cell-associated proteinase  
A:Reference number: A31372; MUID:88125000; PMID:3257574  
A:Accession: A31372  
A:Molecule type: mRNA  
A:Residues: 1-262 <GER>  
A:Cross-references: UNIPROT:P12544; GB:M18737; NID:G184022; PIDN:AAAS2647.1; PID:G306845  
R:Hamed, A.; Lowrey, D.M.; Lichenfeld, M.; Podack, E.R.  
J. Immunol. 141, 3142-3147, 1988  
A:Title: Characterization of three serine esterases isolated from human IL-2 activated killer cells  
A:Reference number: A92823; MUID:89009866; PMID:3262682  
A:Accession: A30525  
A:Molecule type: protein  
A:Residues: 29-40 <HAM>  
R:Kraehenbuehl, O.; Rey, C.; Jenne, D.; Lanzavecchia, A.; Groscurth, P.; Carrel, S.; Tschopp, J.  
J. Immunol. 141, 3471-3477, 1988  
A:Title: Characterization of granzymes A and B isolated from granules of cloned human cytotoxic T-lymphocytes  
A:Reference number: A92824; MUID:89035468; PMID:3263427  
A:Accession: A30526  
A:Molecule type: protein  
A:Residues: 29-39 <KRA>  
R:Poe, M.; Bennett, C.D.; Biddison, W.E.; Blake, J.T.; Norton, G.P.; Rodkey, J.A.; Sigal, J.M.  
J. Biol. Chem. 263, 13215-13222, 1988  
A:Title: Human cytotoxic lymphocyte tryptase. Its purification from granules and the characterization of its substrate specificity  
A:Reference number: A28943; MUID:88330824; PMID:3047119  
A:Accession: A28943  
A:Molecule type: protein  
A:Residues: 29-38, 'RX', '41-46', 'R', '48-49', 'X', '51', 'X', '53' <POE>  
A:Experimental source: CTL line Q31  
A:Note: details from reference A39027 (see entry A61021) suggest this protein is granzyme B  
C:Genetics:  
A:Gene: GDB:GZMA; CTLA3; HPSP  
A:Cross-references: GDB:120601; OMIM:140050  
A:Map position: 5q11-5q12  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: glycoprotein; hydrolase; serine proteinase; T-cell  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-28/Domain: propeptide #status predicted <APT>  
F:29-254/Domain: granzyme A #status experimental <TRY>  
F:54-70,148-218,179-197/Disulfide bonds: #status predicted  
F:69,114,212/Active site: His, Asp, Ser #status predicted  
F:170/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 343.5; DB 1; Length 262;  
Best Local Similarity 35.1%; Pred. No. 3.5e-24;  
Matches 81; Conservative 42; Mismatches 85; Indels 23; Gaps 9;

QY 1 IVGGRARPHAPFVMSVLSQLRGFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60  
DB 29 IIGGNEVTPHSRYPVLLSLDRKTCICAGALIAKDWLTAHC--NLNKRK-QVILGAHSI 85  
QY 61 SRREPTQVFAVQRI-FENGTDVFNLLNDIVILQNGSATINANVOAQLPAQGRRLGNG 119  
DB 86 TREPTKQMLVKKEFPYPCYDPAATREGDKLQLTEKAKINKYVITLHLPKGDDVKFG 145  
QY 120 VQCLAMGWLGRNRIASVQLQELNVTVV--TSLCRSN-----VC--TLVGR 164  
DB 146 TMCQVAGWGRTHNSASWSDTLREVNITIDRVKCNDRNHNPNFVIMNMVCAAGSLRGGR 205  
QY 165 QAGVCFDGSGLVNCGLIHGIAFP--VRGCGASGLYPDAPAPA--QFVNW 213  
DB 206 DS--CNGDGSGLPCGVFRGVTSFGLNCKDPRGPGVYLLSKKHLNWI 254

RESULT 12  
156220  
tryptase 2 - rat

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I56220  
R:Sayers, T.J.; Wiltrout, T.A.; Smyth, M.J.; Ottaway, K.S.; Pilaro, A.M.; Sowder, R.; Her  
J. Immunol. 152, 2289-2297, 1994  
A:Title: Purification and cloning of a novel serine protease, RNK-Tryp-2, from the granu  
A:Reference number: I56220; MUID:94179809; PMID:8133042  
A:Accession: I56220  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-258 <RES>  
A:Cross-references: UNIPROT:P49864; GB:I19694; NID:G487878; PIDN:AAA42057.1; PID:G487879  
C:Superfamily: trypsin; trypsin homology  
F:26-248/Domain: trypsin homology <TRY>

Query Match 29.9%; Score 341; DB 2; Length 258;  
Best Local Similarity 33.5%; Pred. No. 5.8e-24;  
Matches 80; Conservative 46; Mismatches 75; Indels 38; Gaps 10;

QY 1 IVGGRARPHAPFVMSVLSQLRGFCGATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60  
DB 26 IIGGREVQPHSRPFMASIQYRGKHCICGGVLIHPQWVLTAAHCYSRGH--SPTVVLGAHSL 83  
QY 61 SRREPTQVFAVQRI-----FENGTDVFNLLNDIVILQNGSATINANVOAQLPAQGR 115  
DB 84 SKNEPMKQTFEIKBFIPFSGFKSGT-----NDIMLIKLTAAELNKHVQLLHLRSK-NY 136  
QY 116 LQNGVQCLAMGWLGRN-RGTVASVQLQELNVTVTSLCRRSN-----VCT 159  
DB 137 IRDGTQKCVTGSGTKPDVLTTSDLQEVTVIISR--KRCNSQSYNHKPVITKDMICA 194  
QY 160 LVGRQAGVCFDGSGLVNCGLIHGIAFVRGG--CASGLYPDAPAPA--QFVNWIDS 215  
DB 195 GDRGEKDSCKDGGPLICKGVFHALVS--GGYKCGISNKGVVTLTKKYQVWIKS 250

RESULT 13  
S69370  
duodenase - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: S69370  
R:Zamolodchikova, T.S.; Vorotyntseva, T.I.; Nazimov, I.V.; Grishina, G.A.  
Eur. J. Biochem. 227, 873-879, 1995  
A:Title: Duodenase, a new serine protease of unusual specificity from bovine duodenal mu  
A:Reference number: S69370; MUID:95172076; PMID:7867649  
A:Accession: S69370  
A:Molecule type: protein  
A:Residues: 1-226 <ZAM>  
A:Cross-references: UNIPROT:P80219  
C:Superfamily: trypsin; trypsin homology  
F:1-218/Domain: trypsin homology <TRY>

Query Match 29.9%; Score 340.5; DB 2; Length 226;  
Best Local Similarity 34.8%; Pred. No. 5.5e-24;  
Matches 80; Conservative 37; Mismatches 92; Indels 21; Gaps 6;

QY 1 IVGGRARPHAPFVMSVLSQLR--GSHFCGATLIAPNFVMSAAHCVANVAVRVVLGA 57  
DB 1 IIGGHEAKPHSRPYMAFLFKTSKGSHICGGFLVEDFVLTAAHCLGSLN-----VTLGA 55  
QY 58 HNLSRREPTQVFAVQRI-FENGTDVFNLLNDIVILQNGSATINANVOAQLPAQGRRL 116  
DB 56 HNIMERERQQVIVPVRPPIPHDPYNDETLANDIMLLKLTARKADITDKVSPINLPRSLAEV 115  
QY 117 GNGVQCLAMGWLGRNRIASVQLQELNVTVTS---LCRRSN-----VCTLVGRQAG 167  
DB 116 KPMNMCVAGWGRVGNMPSDQLQEDVLEQSEKCIARFNKYIPFTQICAGDPKSRN 175  
QY 168 VCFDGSGLVNCGLIHGIAFVRGGASGLYPDAPAPA--QFVNWIDSII 217  
DB 176 SFGSDGGLVNCVAGQIVSY---GKNDGTTDPDVYTRISSFLPWIKVM 222

RESULT 14  
A27122  
cathepsin G (EC 3.4.21.20) precursor - human  
N:Alternate names: membrane-associated proteinase, U937 cell; neutrophil cathepsin G  
C:Species: Homo sapiens (man)  
C:Date: 05-Jun-1988 #sequence revision 05-Jun-1988 #text\_change 09-Jul-2004  
C:Accession: A32627; A46471; A37115; S44427; A90031; A94428; A05307  
R:Hohn, P.A.; Popescu, N.C.; Hanson, R.D.; Salvesen, G.; Ley, T.J.  
J. Biol. Chem. 264, 13412-13419, 1989  
A:Title: Genomic organization and chromosomal localization of the human cathepsin G gene  
A:Reference number: A32627; MUID:89340411; PMID:2569462  
A:Accession: A32627  
A:Molecule type: DNA  
A:Residues: 1-255 <H>  
A:Cross-references: UNIPROT:P08311; GB:J04990; NID:G179914; PIDN:AAAS1919.1; PID:G179915  
R:Salvesen, G.; Farley, D.; Shuman, J.; Przybyla, A.; Reilly, C.; Travis, J.  
Biochemistry 26, 2289-2293, 1987  
A:Title: Molecular cloning of human cathepsin G: structural similarity to mast cell and  
A:Reference number: A27122; MUID:87299663; PMID:3304423  
A:Accession: A27122  
A:Molecule type: mRNA  
A:Residues: 1-255 <S>  
A:Cross-references: GB:M16117; NID:G181181; PIDN:AAAS2126.1; PID:G181182  
R:Maizon, C.M.; Villiers, C.L.; Colomb, M.G.  
J. Immunol. 147, 921-926, 1991  
A:Title: Proteolysis of C3 on U937 cell plasma membranes. Purification of cathepsin G.  
A:Reference number: A46471; MUID:91318179; PMID:1861080  
A:Accession: A46471  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 21-30 <M>  
A:Experimental source: monocytic cell line U937  
A>Note: sequence extracted from NCBI backbone (NCBIRP:44940)  
R:Bangalore, N.; Travis, J.; Onunka, V.C.; Pohl, J.; Shafer, W.M.  
J. Biol. Chem. 265, 13584-13588, 1990  
A:Title: Identification of the primary antimicrobial domains in human neutrophil cathepsin G.  
A:Reference number: A37115; MUID:90337964; PMID:2116408  
A:Accession: A37115  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 21-25; 97-103 <BAN>  
R:Avril, L.E.; di Martino-Ferrer, M.; Pignede, G.; Seman, M.; Gauthier, F.  
FEBS Lett. 345, 81-86, 1994  
A:Title: Identification of the U-937 membrane-associated proteinase interacting with the  
A:Reference number: S44427; MUID:94252410; PMID:8194606  
A:Accession: S44427  
A:Molecule type: protein  
A:Residues: 21-52 <AVR>  
A>Note: this protein was demonstrated at the surface of U-937 promonocytic cells; it can  
R:Heck, L.W.; Rostand, K.S.; Hunter, F.A.; Bhowan, A.  
Anal. Biochem. 158, 217-227, 1986  
A:Reference number: A90031; MUID:87097924; PMID:3799965  
A:Accession: A90031  
A:Molecule type: protein  
A:Residues: 21-38, 'E', 40, 'T', 42, 'G', 44-45 <HEC>  
A>Note: residue 41 was not identified  
R:Travis, J.; Giles, P.J.; Porcelli, L.; Reilly, C.F.; Baugh, R.; Powers, J.  
in Protein Degradation in Health and Disease, Ciba Foundation Symposium 75, 51-68, 1980  
A:Reference number: A94428  
A:Accession: A94428  
A:Molecule type: protein  
A:Residues: 21-30, 'R', 32-38, 'E', 40, 'T' <TRA>  
C:Comment: This serine proteinase is found in the azurophil granules of neutrophils and  
C:Genetics:  
A:Gene: GDB:CTSG  
A:Cross-references: GDB:119822; OMIM:116830  
A:Map position: 14q11.2-14q11.2  
A:Introns: 19/1; 68/2; 113/3; 198/3  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: glycoprotein; hydrolase; lysosome; serine proteinase  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-20/Domain: propeptide #status predicted <APT>

F:21-255/Product: cathepsin G #status experimental <MAT>  
F:21-238/Domain: trypsin homology <TRY>  
F:49-65,142-207,172-186/Disulfide bonds: #status predicted  
F:64,108,201/Active site: His, Asp, Ser #status predicted

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Matches 82; Conservative 35; Mismatches 87; Indels 23; Gaps 7;

Qy 1 IVGRRARPHAWPFMVSLQIR---GGHFCGATLIAPNFVMSAHC-VANNVNRAVRVWL 56  
Db 21 IIGRESRPSRPMAYLQIQSPAGSRGGLVREDFVLTAACWGSNIN-----VTLG 75  
Qy 57 AHNLSRREPTQVFAVORIPENGTDVFNLLNDIVILQNLGSAITINANVOVAQLPAQGR 115  
Db 76 AHNLRRENTQOHTARRAITHQYNQRTIQNDIMLLQLSRRVRNRNPNVAPRAQEG 135  
Qy 116 LGNGVQCLAMGWGLLGRNRRGIASVQLQELNTV-----VTSLCRSNVCTLVGRQA 166  
Db 136 LRPGTLCTVAGWGRVSMRRG-TDTLREVQLRVQRDRQCLRIFGSDPRRQICVGRDRERK 194  
Qy 167 GVCRGDSGPLVCLNGLIHGIASFVRGGCASGLYPDAFAPVAQFVNW 213  
Db 195 AAFKGDGSGPLLCNNVAHIVSV---GKSGVPEVETRVSSFLPMI 238

RESULT 15  
I55608  
complement factor D (EC 3.4.21.46) precursor - rat  
N:Alternate names: adipsin; C3 convertase activator; endogenous vascular elastase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004  
A:Accession: I55608; S19275  
R:Zhu, L.; Wigle, D.; Hinek, A.; Kobayashi, J.; Ye, C.; Zuker, M.; Keeley, F.W.  
J. Clin. Invest. 94, 1163-1171, 1994  
A:Title: The endogenous vascular elastase that governs development and progression of mor-  
see comments!  
A:Reference number: I55608; MUID:94365184; PMID:8083356  
A:Accession: I55608  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-263 <RES>  
A:Cross-references: UNIPROT:P32038; GB:S73894; NID:G693721; PIDN:AAB31922.1; PID:G693722  
R:Baker, B.C.; Campbell, C.J.; Grinham, C.J.; Turcatti, G.  
Biochem. J. 279, 775-779, 1991  
A:Title: Purification and partial characterization of rat factor D.  
A:Reference number: S19275; MUID:92061993; PMID:1953671  
A:Accession: S19275  
A:Molecule type: protein  
A:Residues: 26-50, 'X', 52-55 <BAK>  
C:Comment: Unlike its human and mouse counterparts, this molecule is N-glycosylated.  
C:Complex: monomer  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: complement alternate pathway; glycoprotein; hydrolase; plasma; serine protei  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-25/Domain: propeptide #status predicted <PRO>  
F:26-263/Product: adipsin #status predicted <MAT>  
F:26-249/Domain: trypsin homology <TRY>  
F:46,124,256,260/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:51-67,149-215,180-196,205-230/Disulfide bonds: #status predicted  
F:66,115,209/Active site: His, Asp, Ser #status predicted

Query Match 29.7%; Score 338.5; DB 1; Length 263;  
Best Local Similarity 31.3%; Pred. No. 1e-23;  
Matches 73; Conservative 49; Mismatches 90; Indels 21; Gaps 4;

Qy 1 IVGRRARPHAWPFMVSLQIRGGHFCGATLIAPNFVMSAHC-VANNVNRAVRVWLGAHN 59  
Db 26 ILGGQEAHARPYMASVQVNGTHVCGGTLVDQWVLSAHCMDGVTKDQVQVLLGAHS 85  
Qy 60 LSRREPTQVFAVOR-IFENGTDVFNLLNDIVILQNLGSAITINANVOVAQLPAQGRRLGN 118



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Db      86  LSSPEPYKHLVDYQSVVLHFGSRPDSVEDDLMLFKLSHNASLGPHVRPLPLQREDREVKP 145
Qy      119  GVOCLAMGGLGRNRGIASVLQELNVTVVVTSLCRESNVCTL-----VRGR 164
Db      146  GTLCDVAGWGVVTHAGRRPDVLQQLTVSMD-----RNTCNLRTHYHDGAIKMMCAESN 200
Qy      165  QAGVCFGDSGSPVLCNGLIHGIASFVRGGCASGLYPDAFAPVAQFVNWIDSII 217
Db      201  RRDTCRGDSGGPLVCGDAEAVVTWGSRVCGNRRKPGVTRVATYVPWIENVL 253
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Search completed: April 18, 2005, 12:50:12  
Job time : 45 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:28:28 ; Search time 178 Seconds  
(without alignments)  
630.030 Million cell updates/sec

Title: US-10-733-288A-4  
Perfect score: 1140  
Sequence: 1 IVGRRARPHAFWVSLQL.....PDAPAPVAQVNWDSIIQR 219

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1133	99.4	267	1	ELNE_HUMAN	P08246 homo sapien
2	900	78.9	282	2	Q8MDJ1	Q8mjd1 canis famil
3	868.5	76.2	265	2	Q61515	Q61515 mus musculus
4	681	59.7	258	2	Q9GME1	Q9gme1 ornithorhyn
5	657	57.6	145	2	Q6LDP5	Q6ldp5 homo sapien
6	654	57.4	207	2	Q9Z284	Q9z284 mus musculus
7	639.5	56.1	254	2	Q8K597	Q8k597 rattus norv
8	638.5	56.0	256	1	PRN3_HUMAN	P24158 homo sapien
9	637.5	55.9	237	2	Q6LBN2	Q6lbn2 homo sapien
10	635.5	55.7	254	1	PRN3_MOUSE	Q61096 mus musculus
11	579.5	50.8	245	2	Q6DF10	Q6df10 xenopus tro
12	480	42.1	251	1	CAP7_HUMAN	P20160 homo sapien
13	428	37.5	219	1	CAP7_PIG	P80015 sus scrofa
14	390	34.2	264	2	Q8QGF6	Q8qgf6 xenopus lae
15	390	34.2	264	2	Q6GYP5	Q6gyp5 xenopus lae
16	385	33.8	258	2	Q867B0	Q867b0 canis famil
17	380	33.3	265	2	Q66KR6	Q66kr6 xenopus lae
18	379	33.2	266	1	EL1_PIG	P00772 sus scrofa
19	375	32.9	265	2	Q7SYI8	Q7syi8 xenopus lae
20	372	32.6	263	2	Q6UWY2	Q6uwy2 homo sapien
21	367	32.2	285	2	Q6GNG0	Q6gng0 xenopus lae
22	366.5	32.1	268	2	Q9W7Q2	Q9w7q2 paralichthy
23	366	32.1	258	2	Q6ISM6	Q6ism6 homo sapien
24	366	32.1	266	1	EL1_RAT	P00773 rattus norv
25	365	32.0	258	1	EL1_HUMAN	Q9un11 homo sapien
26	359	31.5	266	2	Q91X79	Q91x79 mus musculus
27	357.5	31.4	249	2	Q9W7Q1	Q9w7q1 paralichthy
28	357	31.3	266	2	Q9D936	Q9d936 mus musculus
29	356	31.2	266	1	EL1_BOVIN	Q28153 bos taurus
30	355	31.1	278	2	Q68FN6	Q68fn6 brachydanio
31	354	31.1	266	2	O46644	O46644 macaca fasc

RESULT 1						
ID	ELNE_HUMAN	STANDARD;	PRT;	267	AA.	
AC	P08246: P09649;					
DT	01-AUG-1988 (Rel. 08, Created)					
DT	01-AUG-1988 (Rel. 08, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Leukocyte elastase precursor (EC 3.4.21.37) (Neutrophil elastase) (PMN elastase) (Bone marrow serine protease) (Medullasin).					
GN	Name=ELA2;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=89374820; PubMed=2775493;					
RA	Farley D., Travis J., Salvesen G.;					
RT	"The human neutrophil elastase gene. Analysis of the nucleotide sequence reveals three distinct classes of repetitive DNA.";					
RL	Biol. Chem. Hoppe-Seyler 370:737-744(1989).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=88067782; PubMed=3479752;					
RA	Nakamura H., Okano K., Aoki Y., Shimizu H., Naruto M.;					
RT	"Nucleotide sequence of human bone marrow serine protease (medullasin) gene.";					
RL	Nucleic Acids Res. 15:9601-9601(1987).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=89008342; PubMed=2902087;					
RA	Takahashi H., Nukiwa T., Yoshimura K., Quick C.D., States D.J.,					
RA	Holmes M.D., Whang-Peng J., Knutsen T., Crystal R.G.;					
RT	"Structure of the human neutrophil elastase gene.";					
RL	J. Biol. Chem. 263:14739-14747(1988).					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=90211319; PubMed=2322278;					
RA	Okano K., Aoki Y., Shimizu H., Naruto M.;					
RT	"Functional expression of human leukocyte elastase (HLE)/medullasin in eukaryotic cells.";					
RL	Biochem. Biophys. Res. Commun. 167:1326-1332(1990).					
RN	[5]					
RP	SEQUENCE FROM N.A., AND VARIANTS ILE-219; LEU-257 AND LEU-262.					
RA	Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,					
RA	Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,					
RA	Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;					
RT	"NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";					
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.					
RN	[6]					
RP	SEQUENCE OF 30-267 FROM N.A.					
RX	MEDLINE=88032918; PubMed=2822677;					
RA	Okano K., Aoki Y., Sakurai T., Kajitani M., Kanai S., Shimazu T.,					

Q6dgm4 brachydanio  
P80931 ovis aries  
Q6azc0 brachydanio  
Q7sig3 salmo salar  
Q868r2 homo sapien  
Q9gln2 bos taurus  
P28293 mus musculus  
P12544 homo sapien  
Q6azf9 xenopus lae  
Q8n4e0 homo sapien  
Q86vj5 homo sapien  
P00746 homo sapien  
Q8wbz4 homo sapien  
P49864 rattus norv

## ALIGNMENTS

RA	Shimizu H., Naruto M.;	CC	dominant disease in which blood-cell production from the bone
RT	"Molecular cloning of complementary DNA for human medullasin: an	CC	marrow oscillates with 21-day periodicity. Circulating neutrophils
RT	inflammatory serine protease in bone marrow cells.";	CC	vary between almost normal numbers and zero. During intervals of
RL	J. Biochem. 102:13-16(1987).	CC	neutropenia, affected individuals are at risk for opportunistic
RN	[7]	CC	infection. Monocytes, platelets, lymphocytes and reticulocytes
RP	SEQUENCE OF 75-267 FROM N.A.	CC	also cycle with the same frequency.
RX	MEDLINE=88115408; PubMed=3422232;	CC	-!- SIMILARITY: Belongs to the peptidase S1 family. Elastase
RA	Takahashi H., Nukiwa T., Bassett P., Cystal R.G.;	CC	subfamily.
RT	"Myelomonocytic cell lineage expression of the neutrophil elastase	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RL	gene.";	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RN	J. Biol. Chem. 263:2543-2547(1988).	CC	the European Bioinformatics Institute. There are no restrictions on its
RP	SEQUENCE OF 30-247.	CC	use by non-profit institutions as long as its content is in no way
RX	MEDLINE=87175647; PubMed=3550808;	CC	modified and this statement is not removed. Usage by and for commercial
RA	Sinha S., Watorek W., Karr S., Giles J., Bode W., Travis J.;	CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
RT	"Primary structure of human neutrophil elastase.";	CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
RN	Proc. Natl. Acad. Sci. U.S.A. 84:2228-2232(1987).	CC	-----
RP	SEQUENCE OF 262-267.	DR	EMBL; J03545; AAA52378.1; -
RX	MEDLINE=91315473; PubMed=1859409;	DR	EMBL; Y00477; CRA68537.1; -
RA	Aoki Y., Hase T.;	DR	EMBL; X05875; CRA29299.1; -
RT	"The primary structure and elastinolytic activity of medullasin (a	DR	EMBL; X05875; CRA29300.1; ALT_INIT.
RL	serine protease of bone marrow).";	DR	EMBL; M20203; AAA36359.1; -
RN	Biochem. Biophys. Res. Commun. 178:501-506(1991).	DR	EMBL; M20199; AAA36359.1; JOINED.
RP	PRELIMINARY SEQUENCE OF 30-103.	DR	EMBL; M20200; AAA36359.1; JOINED.
RA	Travis J., Giles P.J., Porcelli L., Reilly C.F., Baugh R., Powers J.;	DR	EMBL; AY596461; AAS89303.1; -
RT	(In) Protein degradation in health and disease, Ciba Foundation	DR	EMBL; M34379; AAA36173.1; -
RL	Symposium, pp.75:51-68, Excerpta Medica, Amsterdam and Oxford (1980).	DR	EMBL; D00187; BAA00128.1; -
RN	[11]	DR	PIR; A31976; ELHUL.
RP	SEQUENCE OF 30-49.	DR	PDB; 1B0F; X-ray; A=30-247.
RX	MEDLINE=89315847; PubMed=2501794;	DR	PDB; 1H1B; X-ray; A/B=30-247.
RA	Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,	DR	PDB; 1HNE; X-ray; E=30-247.
RT	Marra M.N., Seeger M., Nathan C.F.;	DR	PDB; 1PPF; X-ray; E=30-247.
RN	"Antibiotic proteins of human polymorphonuclear leukocytes.";	DR	PDB; 1PPG; X-ray; E=30-247.
RP	Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).	DR	MEROPS; S01.131; -
RN	[12]	DR	Genew; HGNC:3309; ELA2.
RP	X-RAY CRYSTALLOGRAPHY (1.84 ANGSTROMS).	DR	MIM; 130130; -
RA	Navia M.A., McKeever B.M., Springer J.P., Lin T.-Y., Williams H.R.,	DR	GO; GO:0004234; F:macrophage elastase activity; TAS.
RT	Fluder E.M., Dorn C.P., Hoogsteen K.;	DR	InterPro; IPR009003; Pept_Ser_Cys.
RN	"Structure of human neutrophil elastase in complex with a peptide	DR	InterPro; IPR001254; Peptidase S1.
RL	chloromethyl ketone inhibitor at 1.84-A resolution.";	DR	InterPro; IPR001314; Peptidase_S1A.
RP	Proc. Natl. Acad. Sci. U.S.A. 86:7-11(1989).	DR	Fram; PF00889; Trypsin; 1
RN	[13]	DR	PRINTS; PR00722; CHYMOTRYPSIN.
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).	DR	PROSITE; PS00240; TRYPSIN_DOM; 1.
RX	MEDLINE=88271660; PubMed=3391280; DOI=10.1016/0014-5793(88)80118-2;	DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
RA	Wei A.-Z., Mayr I., Bode W.;	DR	PROSITE; PS00135; TRYPSIN_SER; 1.
RT	"The refined 2.3-A crystal structure of human leukocyte elastase in a	KW	3D-structure; Direct protein sequencing; Disease mutation;
RL	complex with a valine chloromethyl ketone inhibitor.";	KW	Glycoprotein; Hydrolase; Polymorphism; Serine protease; Signal.
RN	FEBS Lett. 234:367-373(1988).	FT	SIGNAL 1 27 Potential.
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).	FT	PROPEP 28 29
RX	MEDLINE=87053808; PubMed=3640709;	FT	CHAIN 30 267 Leukocyte elastase.
RA	Bode W., Wei A.-Z., Huber R., Meyer E., Travis J., Neumann S.;	FT	ACT_SITE 117 117 Charge relay system.
RT	"X-ray crystal structure of the complex of human leukocyte elastase	FT	ACT_SITE 202 202 Charge relay system.
RL	(PMN elastase) and the third domain of the turkey ovomucoid	FT	DISULFID 55 71
RN	inhibitor.";	FT	DISULFID 151 208
RP	EMBO J. 5:2453-2458(1986).	FT	DISULFID 181 187
RN	[14]	FT	DISULFID 198 223
RP	VARIANTS CH VAL-32; PHE-177 AND GLN-191.	FT	CARBOHYD 88 88
RX	MEDLINE=20047772; PubMed=10581030; DOI=10.1038/70544;	FT	CARBOHYD 124 124
RA	Horwitz M., Benson K.F., Person R.E., Aprikan A.G., Dale D.C.;	FT	CARBOHYD 173 173
RT	"Mutations in ELA2, encoding neutrophil elastase, define a 21-day	FT	VARIANT 32 32
RN	biological clock in cyclic haematopoiesis.";	FT	VARIANT 177 177
RL	Nat. Genet. 23:433-436(1999).	FT	VARIANT 191 191
CC	-!- FUNCTION: Medullasin modifies the functions of natural killer	FT	VARIANT 219 219
CC	cells, monocytes and granulocytes.	FT	VARIANT 257 257
CC	-!- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin.	FT	VARIANT 262 262
CC	-!- Preferential cleavage: Val- -Xaa > Ala- -Xaa.		
CC	-!- TISSUE SPECIFICITY: Bone marrow cells.		
CC	-!- DISEASES: Defects in ELA2 are a cause of cyclic haematopoiesis (CH)		
CC	[MIM:162800]; also known as cyclic neutropenia. CH is an autosomal		

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FT FT CONFLICT 107 107 /FTID=VAR_019239.
N -> D (in Ref. 7).

Query Match 99.4%; Score 1133; DB 1; Length 267;
Best Local Similarity 99.5%; Pred. No. 2.1e-94;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGRARPHAWPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 60
Db IVGGRARPHAWPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 89
QY 61 SRREPTRQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 120
Db SRREPTRQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 149
QY 121 QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSLVCN 180
Db QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSLVCN 209
QY 181 GLIHGIASFVRGCGASGLYPDAPAPVAQFVNWIDSIIOR 219
Db GLIHGIASFVRGCGASGLYPDAPAPVAQFVNWIDSIIOR 248

RESULT 2
Q8MJD1 PRELIMINARY; PRT; 282 AA.
ID Q8MJD1
AC Q8MJD1
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Neutrophil elastase.
GN Names=ELA2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2237507; PubMed=12487025;
RA Katen L.J., Aprikyan A.G., Dale D.C., Osborne W.R.A.;
RT "Molecular Cloning and Sequencing of the Canine Neutrophil Elastase
CDNA."
RL DNA Seq. 13:221-223 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Benson K.F., Albani D., Person R.E., Horwitz M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF494190; AAM95916.1; -.
DR EMBL; AY221639; AAO65978.1; -.
DR PIR; A60551; A60551.
DR HSSP; P08246; 1PPF.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 282 AA; 29920 MW; B6F31953BFA4F9B3 CRC64;

Query Match 78.9%; Score 900; DB 2; Length 282;
Best Local Similarity 77.6%; Pred. No. 2.8e-73;
Matches 170; Conservative 21; Mismatches 28; Indels 0; Gaps 0;
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QY 1 IVGGRARPHAWPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 60
Db IVGGRARPHAWPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 90
QY 61 SRREPTRQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 120
Db GERESTRQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 150
QY 121 QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSLVCN 180
Db QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSLVCN 210
QY 181 GLIHGIASFVRGCGASGLYPDAPAPVAQFVNWIDSIIOR 219
Db GLIHGIASFVRGCGASGLYPDAPAPVAQFVNWIDSIIOR 249

RESULT 3
Q61515 PRELIMINARY; PRT; 265 AA.
ID Q61515
AC Q61515;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Neutrophil elastase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=94309676; PubMed=8035830;
RA Nuchprayoon I., Meyers S., Scott L.M., Suzov J., Hiebert S.;
RA Friedman A.D.;
RT "PEBP2/CBP, the murine homolog of the human myeloid AML1 and PEBP2
beta/CBP beta proto-oncoproteins, regulates the murine myeloperoxidase
and neutrophil elastase genes in immature myeloid cells."
RL Mol. Cell. Biol. 14:5558-5568(1994).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; U04962; AAB60670.1; -.
DR EMBL; U06076; AAB60670.1; JOINED.
DR PIR; I48679; I48679.
DR HSSP; P08246; 1PPF.
DR MEROPS; S01.131; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 265 AA; 28654 MW; 8744D5CE3A72E09D CRC64;

Query Match 76.2%; Score 868.5; DB 2; Length 265;
Best Local Similarity 75.9%; Pred. No. 1.9e-70;
Matches 167; Conservative 19; Mismatches 33; Indels 1; Gaps 1;

QY 1 IVGGRARPHAWPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 60
Db IVGGRARPHAWPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 88
QY 61 SRREPTRQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 120
Db RQERTRQVFAVQRIPENGTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRLNGV 148
QY 121 QCLAMGWLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSLVCN 179
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Db 149 PCLANGWGLGTRSPSPVQLQELNVTVTNMCPRVNVCTLVPRRQAGICFGDGGPLVC 208
QY 180 NGLIHGIAFVGGCAGSLGYPDAFAPVAFVFNWIDSIOR 219
Db 209 NNLVQGIDSFIRGGCGSLGYPDAFAPVAFVFNWIDSIOR 248

RESULT 4
Q9GME1 PRELIMINARY; PRT; 258 AA.
AC Q9GME1; MEDLINE=89076526; PubMed=2462434;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE N-elastase.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; PubMed=11132153; DOI=10.1007/s002510000246;
RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a
monotreme, the platypus, Ornithorhynchus anatinus."
RL Immunogenetics 52:19-28 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Poorafshar M.N.
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF275652; AAG00451.1; -.
DR HSSP; P20160; 1A7S.
DR MEROPS; S01.131; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept Ser Cys.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Protease; Serine protease.
SQ SEQUENCE 258 AA; 28165 MW; 2E1752C300A36138 CRC64;

Query Match 59.7%; Score 681; DB 2; Length 258;
Best Local Similarity 58.7%; Pred. No. 1.7e-53;
Matches 131; Conservative 38; Mismatches 44; Indels 10; Gaps 4;

QY 1 IVGGRRARPHAFVMSVLSL -RGHFPGATLIAPNFVMSAAHCVANVRVVLGAHN 59
Db 24 IVGAVMLFPLA -PYIASLQRNRGGHFCGGTLIHQOFVMTAAHCINSRNVRSVRVVLGAHN 82
QY 60 LSRRETRQVAFVORFENGTDVNLNDIVILQNGSATINANVQVQLPAQRRRLNG 119
Db 83 LRAQESTRQYTSVDQIFENGFSPTQLNDILLVLSRPVTLNANVQLARLPQONQVSG 142
QY 120 VQCLAMGWGLLGNRGI ---ASVQLQELNVTVTSLCRSNVCTLVGRQAGVCFDGGSP 176
Db 143 TQCLAMGWG ---KAIIPAHLIQLQELNVTVTNTQCRNIITLVPSRRAGICFGDGGSP 197
QY 177 LVNGLIHGIAFVGGCAGSLGYPDAFAPVAFVFNWIDSIOR 219
Db 198 LVNCGIVHGDVDFVGGCAGSLGYPDAFAPVAFVFNWIDSIOR 240

RESULT 5
Q6LDP5 PRELIMINARY; PRT; 145 AA.
AC Q6LDP5; MEDLINE=89076526; PubMed=2462434;
DT 03-JUL-2004 (T-EMBLrel. 27, Created)
DT 03-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Neutrophil elastase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89076526; PubMed=2462434;
RA Farley D., Salvessen G.S., Travis J.;
RT "Molecular cloning of human neutrophil elastase."
RL Biol. Chem. Hoppe-Seyler 369:3-7 (1988).
DR EMBL; M27783; AAA35792.1; -.
DR HSSP; P08246; 1B0F.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR009003; Pept Ser Cys.
DR Pfam; PF00089; Trypsin_1; 1.
DR SMART; SM00020; TRYD SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydroxylase; Protease; Serine protease.
FT NON_TER 1
FT CHAIN <1 125 Potential.
SQ SEQUENCE 145 AA; 15278 MW; 9ABE1141003AB00D CRC64;

Query Match 57.6%; Score 657; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.4e-51;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 LINGSATINANVQVQLPAQRRRLNGVQCLAMGWLGRNNGIASVQLQELNVTVTSLCR 153
Db 1 LINGSATINANVQVQLPAQRRRLNGVQCLAMGWLGRNNGIASVQLQELNVTVTSLCR 60
QY 154 RSNVCTLVGRQAGVCFDGGSPPLVNCGLIHGIAFVGGCAGSLGYPDAFAPVAFVFNW 213
Db 61 RSNVCTLVGRQAGVCFDGGSPPLVNCGLIHGIAFVGGCAGSLGYPDAFAPVAFVFNW 120

QY 214 DSIQOR 219
Db 121 DSIQOR 126

RESULT 6
Q9Z284 PRELIMINARY; PRT; 207 AA.
AC Q9Z284; MEDLINE=129/SVJ;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Neutrophil elastase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
RA Sturrock A., Franklin K.F., Wu S.Q., Hoidal J.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF082186; AAC79702.1; -.
DR HSSP; P08246; 1PPF.
DR MEROPS; S01.131; -.
DR MGD; MGI:95316; Ela2.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
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DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM0020; TRYP_SPC; 1.
DR PROSITE: PS00240; TRYP_SIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 207 AA; 2526 MW; 1F4B834DD173DEE CRC64;

Query Match
Best Local Similarity 57.4%; Score 654; DB 2; Length 207;
Matches 131; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

QY 1 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCYANVNVRAVRVVLGNHL 60
DB 1 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCYANVNVRAVRVVLGNHL 60
QY 29 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCYANVNVRAVRVVLGNHL 87
DB 29 IVGGRARPHAWPMVSLQRLGCGATLIAPNFVMSAAHCYANVNVRAVRVVLGNHL 87
QY 61 SRREPTRQVAVORIFENGTDVFNLLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 120
DB 61 SRREPTRQVAVORIFENGTDVFNLLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 120
QY 88 RQERTQTFVSQRIENFGDFPQLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 147
DB 88 RQERTQTFVSQRIENFGDFPQLNDIVILQNGSATINANVQVAPLPAQGRRLNGV 147
QY 121 QCLAMGWGLLGRNGIASVLOELNVVTVSLC-RRSNVCTLVGRGAGVCF 170
DB 121 QCLAMGWGLLGRNGIASVLOELNVVTVSLC-RRSNVCTLVGRGAGVCF 170
QY 148 PCLAMGWGLLGRNGIASVLOELNVVTVSLC-RRSNVCTLVGRGAGVCF 198
DB 148 PCLAMGWGLLGRNGIASVLOELNVVTVSLC-RRSNVCTLVGRGAGVCF 198

RESULT 7
Q8K597 PRELIMINARY; PRT; 254 AA.
ID AC Q8K597;
DC Q8K597;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Proteinase 3 (EC 3.4.21.76).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Rao N.V., Rao G.N., Hoidal J.R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF503440; AA27444.1; -.
DR HSSP; P18291; 1F18.
DR GO: 0004263; F:chymotrypsin activity; IEA.
DR GO: 0008233; F:peptidase activity; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYP_SIN_DOM; 1.
DR PROSITE; PS00134; TRYP_SIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYP_SIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 254 AA; 27682 MW; CA13F453FAF45192 CRC64;

Query Match
Best Local Similarity 56.1%; Score 639.5; DB 2; Length 254;
Matches 121; Conservative 33; Mismatches 64; Indels 3; Gaps 1;

QY 1 IVGGRARPHAWPMVSLQRL- - -GGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGA 57
DB 1 IVGGRARPHAWPMVSLQRL- - -GGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGA 57
QY 30 IVGGRARPHAWPMVSLQRLSPGSHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGA 89
DB 30 IVGGRARPHAWPMVSLQRLSPGSHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGA 89
QY 58 HNLURRPTQVAVORIFENGTDVFNLLNDIVILQNGSATINANVQVAPLPAQGRRLG 117
DB 58 HNLURRPTQVAVORIFENGTDVFNLLNDIVILQNGSATINANVQVAPLPAQGRRLG 117

Db 90 HDLLSEPEQOKFTITQVFENNYPETLNDVLLQLNRPASLGKQVAVASLPQDQSL 149
QY 118 NGVOCLAMGWGLLGRNGIASVLOELNVVTVSLCRRSNVCTLVGRGAGVCFGDSGPL 177
DB 150 QGTQCLAMGWGLLGRNGIASVLOELNVVTVSLCRRSNVCTLVGRGAGVCFGDSGPL 209
QY 178 VCNGLIHGIASFVRGCGCASGLYDPAPFAVQFVNWIDSIQ 218
DB 210 ICNGLIHGVDSFVIRECASLQFPDFPFAVSMYVNIHSLR 250

RESULT 8
PRN3_HUMAN STANDARD; PRT; 256 AA.
ID AC P24158; P15637; P18078; Q9UO08;
DC 01-APR-1990 (Rel. 14, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Myeloblastin precursor (EC 3.4.21.76) (Leukocyte proteinase 3) (PR-3)
DE (PR3) (AGP7) (Wegener's autoantigen) (P29) (C-ANCA antigen)
DE (Neutrophil proteinase 4) (NP-4).
GN Name-PRN3; Synonym=MBN;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Labbaye C., Musette P., Cayre Y.E.;
RL MEDLINE=92021028; PubMed=1681549;
RW "Wegener autoantigen and myeloblastin are encoded by a single mRNA.";
RN [2]
RP SEQUENCE FROM N.A.
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caolice C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dallin E., Dehal P., Denys M., Dettler J.C.,
RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza J., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez P., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RL "The DNA sequence and biology of human chromosome 19.";
RN Nature 428:529-535(2004).
RP [3]
RP SEQUENCE OF 2-256 FROM N.A., AND SEQUENCE OF 48-71 AND 156-181.
RX MEDLINE=91079774; PubMed=2258701;
RA Campanelli D., Melchior M., Fu Y., Nakata M., Shuman H., Nathan C.,
RA Gabay J.E.;
RT "Cloning of cDNA for proteinase 3: a serine protease, antibiotic, and
RT autoantigen from human neutrophils.";
RL J. Exp. Med. 172:1709-1715(1990).
RN [4]
RP SEQUENCE OF 1-20 AND 22-256 FROM N.A.
RX MEDLINE=92390417; PubMed=1518849;
RA Zimmer M., Medcalf R.L., Fink T.M., Mattmann C., Lichter P.,
RA Jenne D.E.;
RT "Three human elastase-like genes coordinately expressed in the
RT myelomonocyte lineage are organized as a single genetic locus on
RT 19pter.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8215-8219(1992).
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CC

[5] SEQUENCE OF 1-200 FROM N.A., AND VARIANT ILE-119.  
 RP MEDLINE=99123768; PubMed=994693;  
 RA Clave E., Mollard J., Hensel N., Raptis A., Barrett A.J.;  
 RT "Donor-recipient polymorphism of the proteinase 3 gene: a potential target for T-cell alloresponses to myeloid leukemia.";  
 RL J. Immunother. 22:1-6(1999).  
 [6] SEQUENCE OF 42-256 FROM N.A.  
 RP MEDLINE=90090622; PubMed=2598267; DOI=10.1016/0092-8674(99)90752-6;  
 RA Bories D., Raynal M.-C., Solomon D.H., Darzynkiewicz Z., Cayre Y.E.;  
 RT "Down-regulation of a serine protease, myeloblastin, causes growth arrest and differentiation of promyelocytic leukemia cells.";  
 RL Cell 59:959-968(1989).  
 [7] SEQUENCE OF 28-67 AND 228-244.  
 RP MEDLINE=91236723; PubMed=2033050;  
 RA Rao N.V., Wehner N.G., Marshall B.C., Gray W.R., Gray B.H.,  
 RT "Characterization of proteinase-3 (PR-3), a neutrophil serine proteinase. Structural and functional properties.";  
 RL J. Biol. Chem. 266:9540-9548(1991).  
 [8] SEQUENCE OF 28-52.  
 RP MEDLINE=91025622; PubMed=2121162;  
 RA Ohlsson K., Linder C., Rosengren M.;  
 RT "Monoclonal antibodies specific for neutrophil proteinase 4. Production and use for isolation of the enzyme.";  
 RL Biol. Chem. Hoppe-Seyler 371:549-555(1990).  
 [9] SEQUENCE OF 28-47.  
 RP MEDLINE=89315847; PubMed=2501794;  
 RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,  
 RA Marra M.N., Seeger M., Nathan C.F.;  
 RT "Antibiotic proteins of human polymorphonuclear leukocytes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).  
 [10] SEQUENCE OF 28-47 AND 196-219.  
 RP MEDLINE=90130450; PubMed=2404977;  
 RA Wilde C.G., Snable J.L., Griffith J.E., Scott R.W.;  
 RT "Characterization of two azurophil granule proteases with active-site homology to neutrophil elastase.";  
 RL J. Biol. Chem. 265:2038-2041(1990).  
 [11] SEQUENCE OF 28-48, AND IDENTITY OF WEGENER'S AUTOANTIGEN WITH PR-3.  
 RP MEDLINE=9032035; PubMed=2377228; DOI=10.1038/346520a0;  
 RA Jenne D.E., Tschopp J., Luedemann J., Utecht B., Gross W.L.;  
 RT "Wegener's autoantigen decoded.";  
 RL Nature 346:520-520(1990).  
 [12] IDENTITY OF WEGENER'S AUTOANTIGEN WITH PROTEINASE 3.  
 RP MEDLINE=91055123; PubMed=2242436;  
 RA Gupta S.K., Niles J.L., McCluskey R.T., Arnaut M.A.;  
 RT "Identity of Wegener's autoantigen (p29) with proteinase 3 and myeloblastin.";  
 RL Blood 76:2162-2162(1990).  
 [13] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RP MEDLINE=96346178; PubMed=8757293; DOI=10.1006/jmbi.1996.0458;  
 RA Fujinaga M., Charnia M.M., Halenbeck R., Koths K., James M.N.G.;  
 RT "The crystal structure of PR3, a neutrophil serine proteinase antigen of Wegener's granulomatosis antibodies.";  
 RL J. Mol. Biol. 261:267-278(1996).  
 CC -1- FUNCTION: Polymorphonuclear leukocyte serine protease that degrades elastin, fibronectin, laminin, vitronectin, and collagen types I, III, and IV (in vitro) and causes emphysema when administered by tracheal insufflation to hamsters.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin, by preferential cleavage: Ala-Xaa > Val-Xaa.  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Elastase subfamily.  
 CC

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EMBL; X56132; CAA39598.1; --  
 DR EMBL; AC004799; -- NOT ANNOTATED\_CDS.  
 DR EMBL; M75154; AAB59558.1; --  
 DR EMBL; M96839; AAB59493.1; --  
 DR EMBL; M96838; AAB59493.1; JOINED.  
 DR EMBL; M96837; AAB59493.1; JOINED.  
 DR EMBL; X55668; CAA39203.1; --  
 DR EMBL; M29142; AAB36342.1; --  
 DR EMBL; AF015449; AAD21524.1; --  
 DR EMBL; AF015446; AAD21524.1; JOINED.  
 DR EMBL; AF015447; AAD21524.1; JOINED.  
 DR EMBL; AF015448; AAD21524.1; JOINED.  
 DR EMBL; M96628; AAB59364.1; --  
 DR PIR; A45080; PRHU3.  
 DR PDB; 1FUJ; X-ray; A/B/C/D=28-248.  
 DR MEROPS; S01.134; --  
 DR Genew; HGNC:9495; PRN3.  
 DR MIM; 177020; --  
 DR GO; GO:0008236; F:serine-type peptidase activity; NAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; Trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW 3D-structure; Collagen degradation; Direct protein sequencing;  
 KW Glycoprotein; Hydrolase; Polymorphism; Serine protease; Signal;  
 KW Zymogen.  
 FT SIGNAL 1 25  
 FT PROPEP 26 27  
 FT CHAIN 28 248  
 FT PROPEP 249 256  
 FT ACT\_SITE 71 71  
 FT ACT\_SITE 118 118  
 FT ACT\_SITE 203 203  
 FT CARBOHYD 129 129  
 FT CARBOHYD 174 174  
 FT DISULFID 56 72  
 FT DISULFID 152 209  
 FT DISULFID 182 188  
 FT DISULFID 199 224  
 FT VARIANT 119 119  
 FT VARIANT 135 135  
 FT VARIANT 136 136  
 FT CONFLICT 2 2  
 FT CONFLICT 46 46  
 FT CONFLICT 48 48  
 FT CONFLICT 64 64  
 FT CONFLICT 70 70  
 FT CONFLICT 255 255  
 FT STRAND 29 29  
 FT STRAND 32 33  
 FT STRAND 36 37  
 FT TURN 40 41  
 Myeloblastin.  
 Charge relay system.  
 Charge relay system.  
 Charge relay system.  
 N-linked (GlcNAc...) (Potential).  
 N-linked (GlcNAc...)  
 V -> I (in dbSNP:351111).  
 A -> T (in dbSNP:1042281).  
 T -> S (in dbSNP:1042282).  
 FTId=VAR\_011691.  
 FTId=VAR\_011713.  
 FTId=VAR\_011714.  
 A -> R (in Ref. 3).  
 Q -> E (in Ref. 9 and 10).  
 R -> A (in Ref. 8).  
 S -> D (in Ref. 7).  
 A -> P (in Ref. 1).  
 Missing (in Ref. 3).

Query Match 56.0%; Score 638.5; DB 1; Length 256;  
 Best Local Similarity 54.1%; Pred. No. 1.2e-49;  
 Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

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QY 1 IVGGRARPHAFPMVSLQLR---GGHFCGATLIAPFVMSAAHCVANVNVRAVRVVLGA 57
DB 28 IVGGHQAQPHSRPYMASLQVRGNPGSHFGCGTLIHPSFVLTAHCLRDIPQRLVNVVLGA 87
QY 58 HNLSREPTQVFAVORIFENGTDPNVLLNDIVILQNGSATINANVQVQLPAQCRRLG 117
DB 88 HNVRTQEPQQHFSVAQVFLNNYDAENKUNLDVLIQLSSPANUSASVATVQLPQQQPPV 147
QY 118 NGVQCLAMGWLGRNRGSIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSP 177
DB 148 HGTCQCLAMGWGRVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 207
QY 178 VCNGLIHGTASFVRGCGASGLYPDAPAPVAQFVNWIDSIOR 219
DB 208 ICDGIIQIGDSFVINGCATRLFPDFTRVALYVDWIRSTLR 249
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## RESULT 9

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Q6LBN2 PRELIMINARY; PRT; 237 AA.
AC Q6LBN2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Proteinase 3 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
SEQUENCE FROM N.A.
RX MEDLINE=90332035; PubMed=2377228; DOI=10.1038/346520a0;
RA Jenne D.E., Tschoep J., Ludemann J., Utecht B., Gross W.L.;
RT "Wegener's autoantigen decoded.";
RL Nature 346:520-520 (1990).
RN [2]
SEQUENCE FROM N.A.
RA Jenne D.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; X56132; CAA39597.1; -.
DR HSSP; P20160; 1A7S.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
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FT NON_TER 1 1
FT SIGNAL <1 6 Potential.
FT CHAIN 9 237 Potential.
SQ SEQUENCE 237 AA; 25884 MW; 38ECA16F6BCD292 CRC64;
Query Match 55.9%; Score 637.5; DB 2; Length 237;
Best Local Similarity 54.5%; Pred. NO. 1.4e-49;
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;
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QY 1 IVGGRARPHAFPMVSLQLR---GGHFCGATLIAPFVMSAAHCVANVNVRAVRVVLGA 57
DB 9 IVGGHQAQPHSRPYMASLQVRGNPGSHFGCGTLIHPSFVLTAHCLRDIPQRLVNVVLGA 68
QY 58 HNLSREPTQVFAVORIFENGTDPNVLLNDIVILQNGSATINANVQVQLPAQCRRLG 117
DB 69 HNVRTQEPQQHFSVAQVFLNNYDAENKUNLDVLIQLSSPANUSASVATVQLPQQQPPV 128
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QY 118 NGVQCLAMGWLGRNRGSIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFGDSGSP 177
DB 129 HGTCQCLAMGWGRVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 188
QY 178 VCNGLIHGTASFVRGCGASGLYPDAPAPVAQFVNWIDSIOR 219
DB 189 ICDGIIQIGDSFVINGCATRLFPDFTRVALYVDWIRSTLR 230
RESULT 10
PRN3 MOUSE STANDARD; PRT; 254 AA.
AC Q61096; O08809;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Myeloblastin precursor (EC 3.4.21.76) (Proteinase 3) (PR-3).
GN Name=PrtN3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=99126347; PubMed=9925946;
RA Sturrock A., Franklin K.P., Wu S.-Q., Hoidal J.R.;
RT "Characterization and localization of the genes for mouse proteinase-3 (PrtN3) and neutrophil elastase (Ela2).";
RL Cytogenet. Cell Genet. 83:104-108 (1998).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97330929; PubMed=9187364; DOI=10.1016/S0014-5793(97)00418-3;
RA Jenne D.E., Froehlich L., Hummel A.M., Specks U.;
RT "Cloning and functional expression of the murine homologue of proteinase 3: implications for the design of murine models of RT vasculitis.";
RL FEBS Lett. 408:187-190 (1997).
RN [3]
SEQUENCE OF 2-254 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=97362044; PubMed=9211743; DOI=10.1007/s002510050260;
RA Aveskog M., Lutzelschwab C., Huang M.R., Hellman L.;
RT "Characterization of cDNA clones encoding mouse proteinase 3 (myeloblastin) and cathepsin G.";
RL Immunogenetics 46:181-191 (1997).
CC -!- FUNCTION: Polymorphonuclear leukocyte serine protease that degrades elastin, fibronectin, laminin, vitronectin, and collagen types I, III, and IV (in vitro) and causes emphysema when administered by tracheal insufflation to hamsters (By similarity).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin, by preferential cleavage: Ala-Xaa-Val-Xaa.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Elastase subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as the content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL; AF082186; AAC7901.1; -.
CC EMBL; U97073; AAB58055.1; -.
CC EMBL; U45325; AAB67271.1; -.
CC HSSP; P18291; 1F18.
CC MEROPS; S01.134; -.
CC MGD; MGI:891580; Prtn3.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinaki M.I., Skalska U., Smalusz D.E., Schmerch A., Schein J.E.,  
RA Jones S.J., Maria M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN SEQUENCE FROM N.A.  
RN TISSUE=Whole body;  
RC Klein S., Gerhard D.S.;  
RC Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
EMBL; BC076933; AAH76933.1; -  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR Pfam; PF00089; Trypsin\_1-  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS02040; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOW\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 245 AA; 26530 MW; B982EA7CA4613EF2 CRC64;  
  
Query Match 50.8%; Score 579.5; DB 2; Length 245;  
Best Local Similarity 52.3%; Pred. No. 2.6e-44; Indels 1; Gaps 1;  
Matches 114; Conservative 33; Mismatches 70;  
  
QY 1 IVGGRRAPHPMPVSLQLR--GGHFCGATLIAPNFVMSAAHCVANNVRAVRVVLGA 60  
DB 26 IVGGREATPNHPYIASIQLRHFHFCGSLIAPQFLMTAAHCVANNVRAVRVVLGA 85  
  
QY 61 SRREPTQVAVORIFENGTPDNLNDIVILQNGSATINNVQVLAQPAQGRRLNGV 120  
DB 86 RANETKQRFVQVFNFGFNPLTLQNDIVILQNGSATINNVQVLAQPAQGRRLNGV 145  
  
QY 121 QCLANGWGLGNGRGVSLQELNVTVV-TSLCRSNVCTLVGRQAGVCFGDSGSLVC 179  
DB 146 QCVTAGWGRSLSTEGQIPRLQELNVTVVTRQNLCPENNICVTGVFMQAGICFGDSGSLVC 205  
  
QY 180 NGLIHGIASFVRGCGAGSLYPPDAFAPVQFVNWIDSII 217  
DB 206 NGVIQGITSFIRSCGNGVTPDFFSRVSFLFRFIDDAI 243  
  
RESULT 12  
CAP7 HUMAN STANDARD; PRT; 251 AA.  
ID CAP7\_HUMAN  
AC P20150; P80014;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Azurocidin precursor (Cationic antimicrobial protein CAP37) (Heparin-  
DE binding protein) (HBP).  
GN Name=AZU1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92013155; PubMed=1919011;  
RA Morgan J.G., Sukienicki T., Pereira H.A., Spitznagel J.K.,  
RA Guerra M.E., Larrick J.L.;  
RA "Cloning of the cDNA for the serine protease homolog CAP37/azurocidin,  
RT

RT a microbicidal and chemotactic protein from human granulocytes.";  
RL J. Immunol. 147:3210-3214(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92390417; PubMed=1518849;  
RA Zimmer M., Medcalf R.L., Fink T.M., Mattmann C., Lichter P.,  
RA Jenne D.E.;  
RT "Three human elastase-like genes coordinately expressed in the  
RT myelomonocyte lineage are organized as a single genetic locus on  
RT 19pter.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:8215-8219(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX PubMed=15057824; DOI=10.1038/nature02399;  
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,  
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,  
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,  
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,  
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,  
RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,  
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,  
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,  
RA Kobayashi A., Lartionov V., Leem S.-H., Lopez P., Lou Y., Lowry S.,  
RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,  
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,  
RA Popkie A.P., Predki P., Quan G., Ramirez L., Raeh S., Retterer J.,  
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,  
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,  
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,  
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,  
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,  
RA Rubin E.M., Lucas S.M.;  
RT "The DNA sequence and biology of human chromosome 19.";  
RL Nature 428:529-535(2004).  
RN [4]  
RP SEQUENCE OF 3-251 FROM N.A.  
RC TISSUE=Neutrophils;  
RX MEDLINE=91264832; PubMed=2049091;  
RA Almeida R.P., Melchior M., Campanelli D., Nathan C., Gabay J.E.;  
RT "Complementary DNA sequence of human neutrophil azurocidin, an  
RT antibiotic with extensive homology to serine proteases.";  
RL Biochem. Biophys. Res. Commun. 177:688-695(1991).  
RN [5]  
RP SEQUENCE OF 27-248.  
RX MEDLINE=91032128; PubMed=2226832; DOI=10.1016/0014-5793(90)80484-Z;  
RA Pohl J., Pereira H.A., Martin N.M., Spitznagel J.K.;  
RT "Amino acid sequence of CAP37, a human neutrophil granule-derived  
RT antibacterial and monocyte-specific chemotactic glycoprotein  
RT structurally similar to neutrophil elastase.";  
RL FEBS Lett. 272:200-204(1990).  
RN [6]  
RP SEQUENCE OF 27-248.  
RC TISSUE=Neutrophils;  
RX MEDLINE=91224149; PubMed=2026172;  
RA Flogaard H., Oesergaard E., Bayne S., Svendsen A., Thomsen J.,  
RA Engels M., Wollmer A.;  
RT "Covalent structure of two novel neutrophil leucocyte-derived  
RT proteins of porcine and human origin. Neutrophil elastase homologues  
RT with strong monocyte and fibroblast chemotactic activities.";  
RL Eur. J. Biochem. 197:535-547(1991).  
RN [7]  
RP SEQUENCE OF 27-47.  
RX MEDLINE=91378304; PubMed=1897955;  
RA Green B.G., Weston H., Ashe B.M., Doherty J., Finke P., Hagmann W.,  
RA Lark M., Mao J., Maycock A., Moore V., Mumford R., Shah S.,  
RA Walakavits L., Knight W.B.;  
RT "PMN elastases: a comparison of the specificity of human isozymes and  
RT the enzyme from other species toward substrates and inhibitors.";  
RL Arch. Biochem. Biophys. 286:284-292(1991).  
RN [8]  
RP SEQUENCE OF 27-46.  
RX MEDLINE=89315847; PubMed=2501794;  
RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,  
Marra M.N., Seeger M., Nathan C.F.;  
RT "Antibiotic proteins of human polymorphonuclear leukocytes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).  
RN [9]  
RP SEQUENCE OF 27-46 AND 194-217.  
RX MEDLINE=90130450; PubMed=2404977;  
RA Wilde C.G., Snable J.L., Griffith J.E., Scott R.W.;  
RT "Characterization of two azurophil granule proteases with active-site  
RT homology to neutrophil elastase.";  
RL J. Biol. Chem. 265:2038-2041(1990).  
RN [10]  
RP SEQUENCE OF 27-67.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90157837; PubMed=2406527; DOI=10.1016/0024-3205(90)90104-Y;  
RA Pereira H.A., Spitznagel J.K., Pohl J., Wilson D.E., Morgan J.,  
RA Palling I., Larrick J.W.;  
RT "CAP 37, a 37 kD human neutrophil granule cationic protein shares  
RT homology with inflammatory proteinases.";  
RL Life Sci. 46:189-196(1990).  
RN [11]  
RP SEQUENCE OF 27-68.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90237224; PubMed=2332502;  
RA Pereira H.A., Shafer W.M., Pohl J., Martin L.E., Spitznagel J.K.;  
RT "CAP37, a human neutrophil-derived chemotactic factor with monocyte  
RT specific activity.";  
RL J. Clin. Invest. 85:1468-1476(1990).  
RN [12]  
RP REVIEW.  
RX MEDLINE=92095171; PubMed=1755383;  
RA Morgan J.G., Pereira H.A., Sukienicki T., Spitznagel J.K.,  
RA Larrick J.W.;  
RT "Human neutrophil granule cationic protein CAP37 is a specific  
RT macrophage chemotaxin that shares homology with inflammatory  
RT proteinases.";  
RL Adv. Exp. Med. Biol. 305:89-96(1991).  
RN [13]  
RP SYNTHESIS OF 46-70.  
RX MEDLINE=93281653; PubMed=8506327;  
RA Pereira H.A., Erdem I., Pohl J., Spitznagel J.K.;  
RT "Synthetic bactericidal peptide based on CAP37: a 37-kDa human  
RT neutrophil granule-associated cationic antimicrobial protein  
RT chemotactic for monocytes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:4733-4737(1993).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RX MEDLINE=97249288; PubMed=9095193;  
RA Iversen L.F., Kastrup J.S., Bjoern S.E., Rasmussen P.B., Wiberg F.C.,  
RA Flogaard H.J., Larsen I.K.;  
RT "Structure of HBP, a multifunctional protein with a serine proteinase  
RT fold.";  
RL Nat. Struct. Biol. 4:265-268(1997).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (1.12 ANGSTROMS).  
RX MEDLINE=98437573; PubMed=9761855; DOI=10.1107/S0907444997016193;  
RA Karlsson S., Iversen L.F., Larsen I.K., Flogaard H.J., Kastrup J.S.;  
RT "Atomic resolution structure of human HBP/CAP37/azurocidin.";  
RL Acta Crystallogr. D 54:598-609(1998).  
RN [16]  
RP FUNCTION: This is a neutrophil granule-derived antibacterial and  
RP monocyte- and fibroblast-specific chemotactic glycoprotein. Binds  
RP heparin. The cytotoxic action is limited to many species of Gram-  
RP negative bacteria; this specificity may be explained by a strong  
RP affinity of the very basic N-terminal half for the negatively  
RP charged lipopolysaccharides that are unique to the Gram-negative  
RP bacterial outer envelope. It may play a role in mediating  
RP recruitment of monocytes in the second wave of inflammation.  
RN [17]  
RP SUBUNIT: Monomer.  
RN [18]  
RP SUBCELLULAR LOCATION: Cytoplasmic granules of neutrophils.  
RN [19]  
RP SIMILARITY: Belongs to the peptidase S1 family. Elastase  
RN subfamily.  
RN [20]  
RP This SWISS-PROT entry is copyright. It is produced through a collaboration  
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EMBL; M96326; AAB59353.1; -  
EMBL; X58794; CAA41601.1; -  
EMBL; AC004799; -; NOT\_ANNOTATED\_CDS.  
PIR; A46268; TRHUZ.  
PDB; 1A7S; X-ray; @=27-251.  
PDB; 1A8S; X-ray; @=27-250.  
PDB; 1FV1; X-ray; A=27-250.  
PDB; 1FV3; X-ray; A=27-250.  
MEROPS; S01.971; -.  
Genew; HGNC:913; AZU1.  
MIM; 162815; -.  
GO; 0042582; C:azurophil granule; IDA.  
GO; 0005576; C:extracellular; NAS.  
GO; 0008201; F:heparin binding; NAS.  
GO; 0015643; P:cellular extravasation; NAS.  
GO; 0045123; P:cellular extravasation; NAS.  
GO; 0050829; P:defense response to Gram-negative bacteria; TAS.  
GO; 0008347; P:glia cell migration; IDA.  
GO; 0050930; P:induction of positive chemotaxis; NAS.  
GO; 0001719; P:inhibition of caspase activation; NAS.  
GO; 0048246; P:macrophage chemotaxis; NAS.  
GO; 0001774; P:macrophage chemotaxis; NAS.  
GO; 0042117; P:monocyte activation; IDA.  
GO; 0045785; P:positive regulation of cell adhesion; IDA.  
GO; 0050754; P:positive regulation of fractalkine biosynth. . ; IDA.  
GO; 0050725; P:positive regulation of interleukin-1 beta b. . ; IDA.  
GO; 0045348; P:positive regulation of MHC class II biosynt. . ; IEP.  
GO; 0050766; P:positive regulation of phagocytosis; IDA.  
GO; 0042535; P:positive regulation of tumor necrosis facto. . ; IDA.  
GO; 0007205; P:protein kinase C activation; TAS.  
Query Match 42.1%; Score 480; DB 1; Length 251;  
Best Local Similarity 45.2%; Pred. No. 2.7e-35;  
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;  
QY 1 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60  
DB 27 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 86  
QY 61 SRRE-PTQVFAVQRIFFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGRRLGNG 119  
DB 87 RRRERQSRQTTSISSMSGYDPOQNLNDMLLDREANLTPSVALVPLPQNTAVEAG 146  
QY 120 VCLAMGGLLRNGRIASVLQELNVTVV-TSLCRSNVCTLVGRQAGVCFDGSGLPLV 178  
DB 147 TRCVAGWSQSRGSLRFRFFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 206  
QY 179 CNGLIHGIAFVGGCAGSLYDPAPVAQFVNWIDSII 217  
DB 207 CEGLAHGVASFSLGFCGRG--PDFFTRVALPRDWIDGVL 243

RESULT 13  
CAP7\_PIG STANDARD; PRT; 219 AA.  
AC PB0015;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Auroidicin (Cationic antimicrobial protein CAP37) (Heparin-binding protein) (HBP).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Neutrophils;  
RX MEDLINE-91224149; PubMed-2026172;  
RA Flodgaard H., Oestergaard E., Bayne S., Svendsen A., Thomsen J.,  
RA Engels M., Wollmer A.;  
RT "Covalent structure of two novel neutrophil leucocyte-derived  
RT proteins of porcine and human origin. Neutrophil elastase homologues  
RT with strong monocyte and fibroblast chemotactic activities.";  
RL Eur. J. Biochem. 197:535-547(1991).  
RN [2].  
RP PARTIAL SEQUENCE, DISULFIDE BONDS, CARBOHYDRATE-LINKAGE SITES ASN-113  
RP AND ASN-144, AND MASS SPECTROMETRY.  
RX PubMed-2076469;  
RA Sorensen H.H., Thomsen J., Bayne S., Højrup P., Roepstorff P.;  
RT "Strategies for determination of disulphide bridges in proteins using  
RT plasma desorption mass spectrometry.";  
RL Biomed. Environ. Mass Spectrom. 19:713-720(1990).  
CC -!- FUNCTION: This is a neutrophil granule-derived antibacterial and  
CC monocyte- and fibroblast-specific chemotactic glycoprotein. Binds  
CC heparin.  
CC -!- SUBUNIT: Monomer.  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Elastase  
CC subfamily.  
CC PIR; S15393; TRPGAZ.  
DR HSRP; P20160; 1A7S.  
DR MEROPS; S01.971; -.  
DR GO; 0042582; C:azurophil granule; ISS.  
DR GO; 0005576; C:extracellular; ISS.  
DR GO; 0008201; F:heparin binding; ISS.  
DR GO; 0015643; P:cellular extravasation; ISS.  
DR GO; 0045123; P:cellular extravasation; ISS.  
DR GO; 0050829; P:defense response to Gram-negative bacteria; ISS.  
DR GO; 0008347; P:glia cell migration; ISS.  
DR GO; 0050930; P:induction of positive chemotaxis; ISS.  
DR GO; 0001719; P:inhibition of caspase activation; ISS.  
DR GO; 0048246; P:macrophage chemotaxis; ISS.  
DR GO; 0001774; P:macrophage chemotaxis; ISS.  
DR GO; 0042117; P:monocyte activation; ISS.  
DR GO; 0045785; P:positive regulation of cell adhesion; ISS.  
DR GO; 0050754; P:positive regulation of fractalkine biosynth. . ; ISS.  
DR GO; 0050725; P:positive regulation of interleukin-1 beta b. . ; ISS.  
DR GO; 0045348; P:positive regulation of MHC class II biosynt. . ; ISS.  
DR GO; 0050766; P:positive regulation of phagocytosis; ISS.  
DR GO; 0042535; P:positive regulation of tumor necrosis facto. . ; ISS.  
DR GO; 0007205; P:protein kinase C activation; ISS.  
DR InterPro; IPR009003; Pept Ser Cys.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00240; TRYPSIN\_HIS; FALSE\_NEG.  
DR PROSITE; PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
DR PROSITE; PS00135; TRYPSIN\_SER; FALSE\_NEG.  
KW Antibiotic; Chemotaxis; Direct protein sequencing; Glycoprotein;  
KW Heparin-binding; Serine protease homolog.  
FT CARBOHYD 113 113 N-linked (GlcNAc. . .).  
FT CARBOHYD 144 144 N-linked (GlcNAc. . .).  
FT DISULFID 26 42  
FT DISULFID 122 179  
FT DISULFID 152 158  
SQ SEQUENCE 219 AA; 24301 MW; 99129CAD88B0749D CRC64;  
Query Match 37.5%; Score 428; DB 1; Length 219;  
Best Local Similarity 41.1%; Pred. No. 1.2e-30;  
Matches 90; Conservative 40; Mismatches 83; Indels 6; Gaps 2;  
QY 1 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60  
DB 1 IVGRRARPHAWPMVSLQRLGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60  
QY 61 SRREPTQVFAVQRIFFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGRRLGNG 120  
DB 61 RQEQSRQTTSIRSIQSGYDPRQNLNDMLLDREANLTPSVALVPLPQNTAVEAGT 120



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13]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RA      Klein S., Strausberg R.;
RC      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL      -1- SIMILARITY: Belongs to peptidase family S1.
DR      EMBL; BC072970; AA472970.1; .
DR      GO: GO:0004263; F:chymotrypsin activity; IEA.
DR      GO: GO:0008233; F:peptidase activity; IEA.
DR      GO: GO:0004295; F:trypsin activity; IEA.
DR      GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR001254; Peptidase_S1.
DR      InterPro; IPR001314; Peptidase_S1A.
DR      InterPro; IPR003003; Pept_Ser_Cys.
DR      Pfam; PF00089; Trypsin; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00020; TRYSPC; 1.
DR      PROSITE; PS02040; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
KW      Hydrolase; Protease; Serine protease.
SQ      SEQUENCE      264 AA;  28066 MW;  1AD1FD9CB43C1A53 CRC64;
Query Match      34.2%;  Score 390;  DB 2;  Length 264;
Best Local Similarity      38.8%;  Pred. No. 4e-27;

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us-10-733-288a-4.rup

Mon Apr 18 13:05:50 2005

Matches		94; Conservative	41; Mismatches	77; Indels	30; Gaps	10;
QY	1	IVGGRARPHAWPFVMSLQLRGG----	HFCGATLIAPNFVMSAAHCVANVVRV--	RVV	54	
Db	28	VIGGSEASRNSWFWQISLQYSSSGSWYHTCGGSLIRANRVMTAAHCVD----	RAVSRYVV	83		
QY	55	LGAHNLSRREPTROVFAVORIFENGTD--	DPVNLN--DIVILQLNGSATINANVQVQLPA	111		
Db	84	VGDNHYQNDGTEQYISVSRIVKHANWPNNTAGGYDIAVLHLASSATLNSYVKLAQLPA	143			
QY	112	QGRRLGNGVQCLAMGWLLGRNRTASVLOELNVTVT-----	SLCRRSNVCTL	160		
Db	144	DGAVLGHNYNCVVTGWGKTSNNGNLASALQOAPLPVVAHATCSSGSGSYWGSTVKSTMVV	CAG	203		
QY	161	VRGRQAGVCEGDSGPLVC--	NGL--IHGIASFV-RGGCAGLYPDAPAPVQFVNWIDS	215		
Db	204	GDGVRSG-CQGDGSGPLNCPVNGVYQVHGVTSFVSSSGCSTYVKPTVTRVSAIYIGWINN	262			
QY	216	II	217			
Db	263	NI	264			

Search completed: April 18, 2005, 12:49:24  
Job time : 181 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:49:34 ; Search time 135 Seconds  
(without alignments)  
539.179 Million cell updates/sec

Title: US-10-733-288A-4

Perfect score: 1140

Sequence: 1 IVGRRRPHAMFVMSLQI.....PDAPVAFVFNWIDSIIR 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 segs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTU8\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	99.4	238	11	US-09-789-210-31
2	1133	99.4	238	16	US-10-408-765A-197
3	1123	98.5	218	16	US-10-408-765A-87
4	1114	97.7	218	9	US-09-861-708-3
5	632.5	55.5	229	11	US-09-789-210-30
6	480	42.1	222	15	US-10-423-311-1
7	480	42.1	225	11	US-09-789-210-32
8	480	42.1	225	17	US-10-868-577A-30
9	480	42.1	251	17	US-10-868-577A-38
10	416	36.5	199	14	US-10-384-474-8
11	414	36.3	199	15	US-10-423-311-2
12	376	33.0	284	9	US-09-888-615-112
13	372	32.6	283	10	US-09-946-374-111

14	372	32.6	283	13	US-10-052-586-272	Sequence 272, App
15	372	32.6	283	14	US-10-174-590-272	Sequence 272, App
16	372	32.6	283	14	US-10-176-758-272	Sequence 272, App
17	372	32.6	283	14	US-10-175-737-272	Sequence 272, App
18	372	32.6	283	14	US-10-174-581-272	Sequence 272, App
19	372	32.6	283	14	US-10-176-483-272	Sequence 272, App
20	372	32.6	283	14	US-10-176-749-272	Sequence 272, App
21	372	32.6	283	14	US-10-176-914-272	Sequence 272, App
22	372	32.6	283	14	US-10-176-915-272	Sequence 272, App
23	372	32.6	283	14	US-10-173-706-272	Sequence 272, App
24	372	32.6	283	14	US-10-175-738-272	Sequence 272, App
25	372	32.6	283	14	US-10-175-752-272	Sequence 272, App
26	372	32.6	283	14	US-10-176-482-272	Sequence 272, App
27	372	32.6	283	14	US-10-176-757-272	Sequence 272, App
28	372	32.6	283	14	US-10-176-913-272	Sequence 272, App
29	372	32.6	283	14	US-10-180-552-272	Sequence 272, App
30	372	32.6	283	14	US-10-180-557-272	Sequence 272, App
31	372	32.6	283	14	US-10-173-700-272	Sequence 272, App
32	372	32.6	283	14	US-10-175-743-272	Sequence 272, App
33	372	32.6	283	14	US-10-174-579-272	Sequence 272, App
34	372	32.6	283	14	US-10-174-582-272	Sequence 272, App
35	372	32.6	283	14	US-10-174-588-272	Sequence 272, App
36	372	32.6	283	14	US-10-175-739-272	Sequence 272, App
37	372	32.6	283	14	US-10-175-740-272	Sequence 272, App
38	372	32.6	283	14	US-10-175-743-272	Sequence 272, App
39	372	32.6	283	14	US-10-176-488-272	Sequence 272, App
40	372	32.6	283	14	US-10-176-492-272	Sequence 272, App
41	372	32.6	283	14	US-10-176-747-272	Sequence 272, App
42	372	32.6	283	14	US-10-176-750-272	Sequence 272, App
43	372	32.6	283	14	US-10-176-985-272	Sequence 272, App
44	372	32.6	283	14	US-10-176-987-272	Sequence 272, App
45	372	32.6	283	14	US-10-176-992-272	Sequence 272, App

#### ALIGNMENTS

#### RESULT 1

US-09-789-210-31  
; Sequence 31, Application US/09789210  
; Publication No. US20040241646A1  
; GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE  
COLPITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
GRANADOS, EDWARD N.  
KLASS, MICHAEL R.  
RUSSELL, JOHN C.  
STEWART, KENT D.  
STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

OF THE PROSTATE

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq For Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/789,210

FILING DATE: 20-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/944,483

FILING DATE: <Unknown>



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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (218)..(218)
; OTHER INFORMATION: Unknown Amino Acid
US-09-861-708-3

Query Match          97.7%; Score 1114; DB 9; Length 218;
Best Local Similarity 99.1%; Pred. No. 6e-108;
Matches 215; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 IVGRRARPHAWPFMVSQLRGCGHFCGATLIAFNFVMSAAHCVANVNVRAVRVVLGAHNL 60
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Db 61 SREPTQVFAVQRIFENGTPDVLNLDIVILQNGSATINANVQVAQLPAQGRRLNGV 120
QY 121 QCLAMGWLGRNREGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 180
Db 121 QCLAMGWLGRNREGIASVLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 180
QY 181 GLIHGIASFVRGGCASGLYPDAFAPVAQFVNWIDSII 217
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RESULT 5
US-09-789-210-30
; Sequence 30, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-789-210-30

Query Match          55.5%; Score 632.5; DB 11; Length 229;
Best Local Similarity 54.1%; Pred. No. 1.2e-57;
Matches 120; Conservative 40; Mismatches 59; Indels 3; Gaps 1;

QY 1 IVGRRARPHAWPFMVSQLR--GGHFCGATLIAFNFVMSAAHCVANVNVRAVRVVLGA 57
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Db 61 HNVRTQEPQQHFSVAQVFLNNYDAENKLDILLIQLSSPALSASVTSVQLPQQQPVP 120
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Db 121 HGTQCLAMGWRGVAHDPPAQVLQELNVTVTFFCPHNICTFVPRKAGICFGDSGGPL 180
QY 178 VCNGLIHGIASFVRGGCASGLYPDAFAPVAQFVNWIDSIIQR 219
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RESULT 6
US-10-423-311-1
; Sequence 1, Application US/10423311
; Publication No. US20030206938A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; APPLICANT: Chodosh, James
; APPLICANT: Callegan, Michelle C.
; TITLE OF INVENTION: TREATMENT AND INHIBITION OF OCULAR INFECTIONS AND WOUNDS BY CAP37
; FILE REFERENCE: CAP37 PEPTIDES
; FILE REFERENCE: 6267.002
; CURRENT APPLICATION NUMBER: US/10/423,311
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/378,295
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-311-1

Query Match          42.1%; Score 480; DB 15; Length 222;
Best Local Similarity 45.2%; Pred. No. 1e-41;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;

QY 1 IVGRRARPHAWPFMVSQLRGCGHFCGATLIAFNFVMSAAHCVANVNVRAVRVVLGAHNL 60
Db 1 IVGRRARPHAWPFMVSQLRGCGHFCGATLIAFNFVMSAAHCVANVNVRAVRVVLGAHNL 60
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Db 61 RRRERQSRQTSISSMSGYDPPQNLNDMLQLDREANLTSSVITLPLQNAIVEAG 120
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Qy 179 CNGLIHGIAFVRGGCASGLYPDAFAPVAQFVNWIDSII 217  
Db 181 CEGLAHGVASFSLGPCGRG--PDFFTRVALFRDWIDGVL 217

RESULT 7  
US-09-789-210-32  
; Sequence 32, Application US/09789210  
; Publication No. US20040241646A1  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; COLPITTS, TRACEY L.  
; FRIEDMAN, PAULA N.  
; GRANADOS, EDWARD N.  
; KLASS, MICHAEL R.  
; RUSSELL, JOHN C.  
; STEWART, KENT D.  
; STROUPE, STEVEN D.  
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
; OF THE PROSTATE  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/789,210  
; FILING DATE: 20-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/944,483  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6183.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 225 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: None  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-789-210-32

Query Match 42.1%; Score 480; DB 11; Length 225;  
Best Local Similarity 45.2%; Pred. No. 1e-41;  
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;  
Qy 1 IVGGRRARHPFVMSLQLRGHCATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60  
Db 1 IVGGRRARHPFVMSLQLRGHCATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60  
Qy 61 SRRE-PTROQVAVQRIFFENGTFDVPVNLNDIVILQNGSATINANVQVQLPAQGRRLNG 119  
Db 61 RRRERQSRQTFSSISMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAIVEAG 120  
Qy 120 VQCLAMGWLLGNRGIASVLQELNVTVV-TSLCRSNVCTLVGRQAGVCFDGSGLV 178  
Db 121 TRCOVAGSGRSGRLSREPRFVNVTVPEDQCRNNVCTGLTRRGICNGDGTPLV 180  
Qy 179 CNGLIHGIAFVRGGCASGLYPDAFAPVAQFVNWIDSII 217  
Db 181 CEGLAHGVASFSLGPCGRG--PDFFTRVALFRDWIDGVL 217  
RESULT 9  
US-10-868-577A-38  
; Sequence 38, Application US/10868577A  
; Publication No. US20050032697A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al.  
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS  
; FILE REFERENCE: 28967/39359A  
; CURRENT APPLICATION NUMBER: US/10/868,577A  
; CURRENT FILING DATE: 2004-06-14  
; PRIOR FILING DATE: 2004-06-14  
; PRIOR APPLICATION NUMBER: US 60/478,390  
; PRIOR FILING DATE: 2003-06-12  
; PRIOR APPLICATION NUMBER: US 10/669,176  
; PRIOR FILING DATE: 2003-09-23  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 38  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-868-577A-38

Qy 179 CNGLIHGIAFVRGGCASGLYPDAFAPVAQFVNWIDSII 217  
Db 181 CEGLAHGVASFSLGPCGRG--PDFFTRVALFRDWIDGVL 217

US-09-789-210-32  
; Sequence 32, Application US/09789210  
; Publication No. US20040241646A1  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; COLPITTS, TRACEY L.  
; FRIEDMAN, PAULA N.  
; GRANADOS, EDWARD N.  
; KLASS, MICHAEL R.  
; RUSSELL, JOHN C.  
; STEWART, KENT D.  
; STROUPE, STEVEN D.  
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
; OF THE PROSTATE  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/789,210  
; FILING DATE: 20-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/944,483  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6183.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 225 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: None  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-789-210-32

Query Match 42.1%; Score 480; DB 11; Length 225;  
Best Local Similarity 45.2%; Pred. No. 1e-41;  
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;  
Qy 1 IVGGRRARHPFVMSLQLRGHCATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60  
Db 1 IVGGRRARHPFVMSLQLRGHCATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60  
Qy 61 SRRE-PTROQVAVQRIFFENGTFDVPVNLNDIVILQNGSATINANVQVQLPAQGRRLNG 119  
Db 61 RRRERQSRQTFSSISMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAIVEAG 120  
Qy 120 VQCLAMGWLLGNRGIASVLQELNVTVV-TSLCRSNVCTLVGRQAGVCFDGSGLV 178



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Query Match 42.1%; Score 480; DB 17; Length 251;
Best Local Similarity 45.2%; Pred. No. 1.2e-41;
Matches 99; Conservative 35; Mismatches 81; Indels 4; Gaps 3;

QY 1 IVGRRARPHAWPFVMSLQRLRGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
DB 27 IVGRRARPHAWPFVMSLQRLRGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 86
QY 61 SRREPTRQVFAVORIFENGTPDVPVNLNDIVILQNGSATINANVQVQALPAQGRRLGNG 119
DB 87 RRRERQSRQTFSSISMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAG 146
QY 120 VQCLANGWLLGNRGIASVLOELNVTIV-TSLCRSNVCTLVGRQAGVCFDGSPLV 178
DB 147 TRCQVAGWGSQRSGRLSPFPFVNVTVTPEDQCRPNNVCTGLTRRGICNGDGTPLV 206
QY 179 CNGLIHGIASVFRGGCASGLYPDAPAPVAQFVNWIDSII 217
DB 207 CEGLAHGVASFSLGPCRG--PDFTRVALFRDWIDGVL 243

RESULT 10
US-10-384-474-8
; Sequence 8, Application US/10384474
; Publication No. US20030170745A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; TITLE OF INVENTION: AN EARLY DETECTION MARKER FOR CHRONIC INFLAMMATORY ASSOCIATED DIS
; FILE REFERENCE: 6267.001
; CURRENT APPLICATION NUMBER: US/10/384,474
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-474-8

Query Match 36.5%; Score 416; DB 14; Length 199;
Best Local Similarity 43.8%; Pred. No. 4.3e-35;
Matches 88; Conservative 31; Mismatches 78; Indels 4; Gaps 3;

QY 19 QLRGSHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL-SRRE-PTROVFAVORIFE 77
DB 1 QNGRHFCCGALIHARFVMTAASCFOQNPQGVSTVILGAYDLRRERQSRQTFSSISMS 60
QY 78 NGTDPVNLNDIVILQNGSATINANVQVQALPAQGRRLGNGVQCLANGWLLGNRNGIA 137
DB 61 NGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAGTRCQVAGWGSQRSGRLS 120
QY 138 SVLOELNVTIV-TSLCRSNVCTLVGRQAGVCFDGSPLVNCGLIHGIASVFRGGCAS 196
DB 121 RPFVNVTVTPEDQCRPNNVCTGLTRRGICNGDGTPLVCEGLAHGVASFSLGPCRG 180
QY 197 GLYPDAPAPVAQFVNWIDSII 217
DB 181 G--PDFTRVALFRDWIDGVL 199

RESULT 11
US-10-423-311-2
; Sequence 2, Application US/10423311
; Publication No. US20030206938A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; APPLICANT: Chodosh, James
; APPLICANT: Callegan, Michelle C.
; TITLE OF INVENTION: TREATMENT AND INHIBITION OF OCULAR INFECTIONS AND WOUNDS BY CAP37
; FILE REFERENCE: 6267.002
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; CURRENT APPLICATION NUMBER: US/10/423,311
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/378,295
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-311-2

Query Match 36.3%; Score 414; DB 15; Length 199;
Best Local Similarity 43.7%; Pred. No. 6.9e-35;
Matches 87; Conservative 31; Mismatches 77; Indels 4; Gaps 3;

QY 21 RCGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL-SRRE-PTROVFAVORIFENG 79
DB 2 QQRHFCGALIHARFVMTAASCFOQNPQGVSTVILGAYDLRRERQSRQTFSSISMSSENG 61
QY 80 TDPVNLNDIVILQNGSATINANVQVQALPAQGRRLGNGVQCLANGWLLGNRNGIASV 139
DB 62 YDPQQLNDMLQLDREANLTSSVTILPLQNAATVEAGTRCQVAGWGSQRSGRLSRF 121
QY 140 LOELNVTIV-TSLCRSNVCTLVGRQAGVCFDGSPLVNCGLIHGIASVFRGGCASGL 198
DB 122 PRFVNVTVTPEDQCRPNNVCTGLTRRGICNGDGTPLVCEGLAHGVASFSLGPCRG- 180
QY 199 YPDAPAPVAQFVNWIDSII 217
DB 181 -PDFTRVALFRDWIDGVL 198

RESULT 12
US-09-888-615-112
; Sequence 112, Application US/09888615
; Patent No. US20020064858A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHASVDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-112

Query Match 33.0%; Score 376; DB 9; Length 284;
Best Local Similarity 36.6%; Pred. No. 1e-30;
Matches 87; Conservative 32; Mismatches 93; Indels 26; Gaps 5;

QY 1 IVGRRARPHAWPFVMSLQRLRGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 60
DB 35 IIGGHEVTPHSRPFYMASVFRGGHCGGFLLRARVWVSAACHCFSHRDLRTGLVVLGAHVL 94
QY 61 SRREPTRQVFAVORIFENG-GTDPVNLNDIVILQNGSATINANVQVQALPAQGRRL- 116
DB 95 STAEPTQQVFGIDALTTPDHPHMTHANDICLLQNGSAVLGPAVGLLRPL--GRRARPP 152
QY 117 GNGVQCLANGWLLGNRNGIASVLOELNVTIV-----VTSLCRSNVCTLV 161
DB 153 TAGTRCRVAGWGFVSDFEELPGLMEAKVRVLDPPVCNCSWKHGLTILMLCTRSG----- 207
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QY 162 RGRQAGVCFDGSPLVNCGLIHGIASFVRGCGASGLYDPDAFAPVAQFVNNWIDSIOR 219  
Db 208 DSHRRGFCGADSGPLVCRNRAHGLVFSFGLMCGDKPTDVTQVSAFVAWIWDVVR 265

RESULT 13  
US-09-946-374-111  
; Sequence 111, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099602  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099642  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099741  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099754  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099763  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
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; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100584  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100627  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100661  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100662  
; PRIOR FILING DATE: 1998-09-16  
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; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100683  
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; PRIOR FILING DATE: 1998-09-17  
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; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
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; PRIOR APPLICATION NUMBER: 60/100930  
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; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307

Query Match	32.6%	Score 372;	DB 10;	Length 283;
Best Local Similarity	36.1%;	Pred.No. 2.6e-30;		
Matches	86;	Conservative 33;	Mismatches 93;	Indels 26; Gaps 5;
QY	1	I VGGRRARPHAWPFMVS LQLRGHFCATL IAPNFMVSAACHVANVAVR VVLGAHNL	60	
	:	: : : : :	:	:
Ddb	34	I UGHEVT PHSR PYMASVRFGQHCGGFILRAKVVWSAAHCFSHRDRITGLVVLGAHVL	93	
	:	: : : : :	:	:
QY	61	SREPTTRQFVAQRIFEN-GTDPVNLLNDIVILQLNGSATINANVVOAQLPAQGRL---	116	
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Db      94  STAEPTQVFGIDALTTHPDVHPMTHANDICLLRLNGSAVLGPAVGLLRLP--GRRARPP 151
Qy      117  GNGVOCLAMGWGLLGRNRGIAVSLQELNVTV-----VTSLCRSRNVCTLV 161
Db      152  TAGTRCRVAGGFFVSDFEELPGLWEAKRVLDPDVCNCSWKGHLLTLMCTRSQ----- 206
Qy      162  RQRQAGVCFGDSGSLPVCNGLIHGIASFVRGGCASGLYPDAFAPVAQFVNWIDSIOR 219
Db      207  DSHRRGFCSDSGGLPVCNRNRAHGLVSFSLGWLCDGPKTDPVYTVQVSFAVAIWDVVRR 264

RESULT 14
US-10-052-586-272
; Sequence 272, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
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; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017

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us-10-733-288a-4.rapb

Mon Apr 18 13:05:49 2005

;; PRIOR FILING DATE: 1997-12-18  
;; PRIOR APPLICATION NUMBER: 60/077450  
;; PRIOR FILING DATE: 1998-03-10  
;; PRIOR APPLICATION NUMBER: 60/077632  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077649  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/078886  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078939  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/079664  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/079786  
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;; PRIOR APPLICATION NUMBER: 60/080107  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080194  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080327  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/080333  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/081049  
;; PRIOR FILING DATE: 1998-04-08  
;; PRIOR APPLICATION NUMBER: 60/081070  
;; PRIOR FILING DATE: 1998-04-08  
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;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-05  
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;; PRIOR APPLICATION NUMBER: 60/088212  
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;; PRIOR APPLICATION NUMBER: 60/088217  
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;; PRIOR FILING DATE: 1998-06-10  
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;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089908

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Best Local Similarity 36.1%; Pred. No. 2.6e-30;  
Matches 86; Conservative 33; Mismatches 93; Indels 26; Gaps 5;

Qy 1 IVGRRARPHAWFMVLSQLRGHFCGATLIAFNFMASAAHCVANVNRVAVVUGAHNL 60

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Db 34 IIGHEVTPHSRPMASVREGGQHCGFLRLARWVVSAAHCFSHRDLRTGLVVLGAHVL 93
Qy 61 SREPTQVFAVQRIEEN-GTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRL--- 116
Db 94 STAEPTQVFGIDALTTHPDYHMTHANDICLLRLNGSAVLGPAVGLLRLP--GRRARPP 151
Qy 117 GNGVQCLAMGWGLGRNRGIASVLQELNVTV-----VTSLCRRSNVCTLV 161
Db 152 TAGTRCRVAGWGFVSDPEELPPGLMEAKVRVLDPDVCNCSWKGHILTLMCTRSRSG---- 206
Qy 162 RGRQAGVCFGDSGLVNCGLIHGIASFVRGGCASGLYDPAPAPVAQFVNMWDSIIQR 219
Db 207 DSHRRGFCSDSGPLVCRNRAHGLVSFSLWCQDPKPTPDVYTQVSAFAVAMWDVVRR 264
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## RESULT 15

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US-10-174-590-272
; Sequence 272, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 272
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-272
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Best Local Similarity 36.1%; Pred. No. 2,6e-30;
Matches 86; Conservative 33; Mismatches 93; Indels 26; Gaps 5;
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Db 34 IIGHEVTPHSRPMASVREGGQHCGFLRLARWVVSAAHCFSHRDLRTGLVVLGAHVL 93
Qy 61 SREPTQVFAVQRIEEN-GTDPVNLNDIVILQNGSATINANVOVAQLPAQGRRL--- 116
Db 94 STAEPTQVFGIDALTTHPDYHMTHANDICLLRLNGSAVLGPAVGLLRLP--GRRARPP 151
Qy 117 GNGVQCLAMGWGLGRNRGIASVLQELNVTV-----VTSLCRRSNVCTLV 161
Db 152 TAGTRCRVAGWGFVSDPEELPPGLMEAKVRVLDPDVCNCSWKGHILTLMCTRSRSG---- 206
Qy 162 RGRQAGVCFGDSGLVNCGLIHGIASFVRGGCASGLYDPAPAPVAQFVNMWDSIIQR 219
Db 207 DSHRRGFCSDSGPLVCRNRAHGLVSFSLWCQDPKPTPDVYTQVSAFAVAMWDVVRR 264
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Job time : 136 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 12:39:38 ; Search time 44 Seconds  
(without alignments)  
478.897 Million cell updates/sec

Title: US-10-733-288A-4  
Perfect score: 1140  
Sequence: 1 IVGGRARPHAWPFVMSLQL.....PDAPAPVQFVWIDSIQR 219

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: Pirl:.\*  
2: Pirl:.\*  
3: Pirl:.\*  
4: Pirl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	99.4	267	1 ELRHUL	leukocyte elastase
2	868.5	76.2	265	2 I48679	neutrophil elastase
3	637.5	55.9	256	1 PRHU3	proteainase 3 (EC 3
4	480	42.1	251	1 TRHUZ	azurocidin precurs
5	438	37.5	219	1 TRPGNZ	azurocidin - pig
6	379	33.2	286	1 ELPG	pancreatic elastas
7	366	32.1	266	1 ELRT1	pancreatic elastas
8	364	31.9	258	4 S70439	pancreatic elastas
9	364	31.9	267	4 A56615	pancreatic elastas
10	344.5	30.2	261	2 S40162	probable pancreati
11	343.5	30.1	262	1 A31372	cathepsin G (EC 3
12	341	29.9	258	2 I56220	granzyme A (EC 3.4
13	340.5	29.9	256	2 S69370	trypsin 2 - rat
14	338.5	29.7	255	2 A27122	duodenase - bovine
15	338.5	29.7	263	1 I55608	cathepsin G (EC 3
16	337	29.6	244	2 A34910	complement factor
17	336.5	29.5	259	1 WMS28	complement factor
18	336.5	29.5	259	2 A28223	pancreatic elastas
19	335	29.4	246	1 DBHU	complement factor
20	332.5	29.2	269	2 B26823	pancreatic elastas
21	332.5	29.2	271	1 ELRT2	pancreatic elastas
22	331.5	29.1	257	2 B45061	granzyme A (EC 3.4
23	331.5	29.1	260	2 A45061	granzyme A (EC 3.4
24	328.5	28.8	249	2 A55634	granzyme M (EC 3.4
25	327.5	28.7	271	2 A25528	chymotrypsin (EC 3
26	326.5	28.6	265	2 T10495	pancreatic elastas
27	325	28.5	236	2 A28566	T-cell suppressor
28	325	28.5	244	2 A46721	chymase (EC 3.4.21
29	322.5	28.3	226	1 KCUF	bradyrin (EC 3.4

mast cell serine p  
pancreatic elastas  
plasmin (EC 3.4.21  
mast cell proteina  
plasmin (EC 3.4.21  
chymase (EC 3.4.21  
serine proteinase  
chymotrypsin (EC 3  
pancreatic elastas  
plasmin (EC 3.4.21  
apoptotain(a) (EC  
plasmin (EC 3.4.21  
pancreatic elastas  
plasmin (EC 3.4.21  
chymase (EC 3.4.21  
pancreatic elastas

## ALIGNMENTS

### RESULT 1

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N;Alternate names: inflammatory serine proteinase; medullasin; neutrophil elastase  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 09-Jul-2004  
C;Accession: A31976; S04954; S06241; A27064; S00631; A28370; A34570; A05293; A25907; S1  
R;Takahashi, H.; Nukiwa, T.; Yoshimura, K.; Quick, C.D.; States, D.J.; Holmes, M.D.; Wh  
J. Biol. Chem. 263, 14739-14747, 1988  
A;Title: Structure of the human neutrophil elastase gene.  
A;Reference number: A31976; MUID:89008342; PMID:2902087  
A;Accession: A31976  
A;Molecule type: DNA  
A;Residues: 1-267 <TAK>  
A;Cross-references: UNIPROT:P08246; GB:M20203; GB:J04032; NID:g189147; PIDN:AAA36359.1;  
R;Farley, D.; Travis, J.; Salvesen, G.  
Biol. Chem. Hoppe-Seyler 370, 737-744, 1989  
A;Title: The human neutrophil elastase gene. Analysis of the nucleotide sequence reveal  
A;Reference number: S04954; MUID:89374820; PMID:2775493  
A;Accession: S04954  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-267 <FAR>  
R;Nakamura, H.; Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.  
Nucleic Acids Res. 15, 9601-9602, 1987  
A;Title: Nucleotide sequence of human bone marrow serine protease (medullasin) gene.  
A;Reference number: S06241; MUID:88067782; PMID:3479752  
A;Accession: S06241  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-267 <NAK>  
A;Cross-references: EMBL:Y00477; NID:g34529; PIDN:CAA68537.1; PID:g296665  
R;Okano, K.; Aoki, Y.; Sakurai, T.; Kajitani, M.; Kanai, S.; Shimazu, T.; Shimizu, H.;  
J. Biochem. 102, 13-16, 1987  
A;Title: Molecular cloning of complementary DNA for human medullasin: an inflammatory s  
A;Reference number: A27064; MUID:88032918; PMID:2822677  
A;Accession: A27064  
A;Molecule type: mRNA  
A;Residues: 30-267 <OKA>  
A;Cross-references: EMBL:X05875; NID:g34532; PIDN:CAA29300.1; PID:g1335212  
R;Farley, D.; Salvesen, G.; Travis, J.  
Biol. Chem. Hoppe-Seyler 369(Suppl.), 3-7, 1988  
A;Title: Molecular cloning of human neutrophil elastase.  
A;Reference number: S00631; MUID:89076526; PMID:2462434  
A;Accession: S00631  
A;Molecule type: mRNA  
A;Residues: 123-267 <FA2>  
A;Cross-references: GB:M27783; NID:g182055; PIDN:AAA35792.1; PID:g182056  
R;Takahashi, H.; Nukiwa, T.; Bassett, P.; Crystal, R.G.  
J. Biol. Chem. 263, 2543-2547, 1988

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A;Title: Myelomonocytic cell lineage expression of the neutrophil elastase gene.  
A;Reference number: A28370; MUID:88115408; PMID:3422232  
A;Accession: A28370  
A;Molecule type: mRNA  
A;Residues: 75-267 <TA2>  
A;Cross-references: GB:J03545; NID:9182050; PIDN:AAA52378.1; PID:g182051  
R;Okano, K.; Aoki, Y.; Shimizu, H.; Naruto, M.  
Biochem. Biophys. Res. Commun. 167, 1326-1332, 1990  
A;Title: Functional expression of human leukocyte elastase (HLE)/medullasin in eukaryotic cells.  
A;Reference number: A34570; MUID:90211319; PMID:3222278  
A;Accession: A34570  
A;Molecule type: mRNA  
A;Residues: 1-267 <OK2>  
A;Cross-references: GB:M4379; NID:9187116; PIDN:AAA36173.1; PID:g307123  
R;Travis, J.; Giles, P.J.; Porcella, L.; Reilly, C.F.; Baugh, R.; Powers, J.  
in Protein Degradation in Health and Disease, Ciba Foundation Symposium 75, 51-68, 1980  
A;Reference number: A94428  
A;Accession: A05293  
A;Molecule type: protein  
A;Residues: 30-66, G, 68-73, D, 75, 78-82, E, 84-89, T, 91-94, P, 97-100, L, 102-103 <TR>  
A;Experimental source: neutrophil granulocytes  
R;Sinha, S.; Watorek, W.; Karr, S.; Giles, J.; Bode, W.; Travis, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 2228-2232, 1987  
A;Title: Primary structure of human neutrophil elastase.  
A;Reference number: A25907; MUID:87175647; PMID:3550808  
A;Accession: A25907  
A;Molecule type: protein  
A;Residues: 30-247 <SIN>  
A;Note: The sequence from Fig. 1 is inconsistent with that from Fig. 2 in having 107-Asp  
R;Green, B.G.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagmann, W.; Lark, M.; Ma  
Arch. Biochem. Biophys. 286, 284-292, 1991  
A;Title: PKN elastases: a comparison of the specificity of human isozymes and the enzyme  
A;Reference number: S14736; MUID:91378304; PMID:1897955  
A;Accession: S14736  
A;Molecule type: protein  
A;Residues: 30-50 <GRE>  
A;Comment: This is a lysosomal proteinase found in the azurophil granules of neutrophils  
C;Comment: This elastase cleaves preferentially bonds after Ala and Val. It is believed  
C;Genetics:  
A;Gene: GDB:ELA2  
A;Cross-references: GDB:118792; OMIM:130130  
A;Map position: 19p13.3-19p13.3  
A;Introns: 23/1; 75/2; 122/3; 199/3  
C;Superfamily: trypsin; trypsin homology  
F;1-27/Domain: signal sequence #status predicted <SIG>  
F;28-29/Domain: propeptide #status predicted <PRO>  
F;30-247/Product: leukocyte elastase #status experimental <MAT>  
F;30-242/Domain: trypsin homology <TRI>  
F;248-267/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;55-71,151-208,181-187,198-223/Disulfide bonds: #status experimental  
F;70,117,202/Active site: His, Asp, Ser #status predicted  
F;68/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;124,173/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.4%; Score 1133; DB 1; Length 267;  
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Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGRARPHAWPFMSQLQRGHFCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 60  
DB 30 IVGGRARPHAWPFMSQLQRGHFCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 89  
QY 61 SRREPTQFAVQRIEFGNDPNNLLNDIVILQNGSATINAVQVLAQRRLLNGV 120  
DB 90 SRREPTQFAVQRIEFGNDPNNLLNDIVILQNGSATINAVQVLAQRRLLNGV 149  
QY 121 QCLAMGWLGRNRIASVQLQELNVTVTSLSLRSSNVCTLVGRQAGVCFGDSGPLVCN 180  
DB 150 QCLAMGWLGRNRIASVQLQELNVTVTSLSLRSSNVCTLVGRQAGVCFGDSGPLVCN 209  
QY 181 GLIHGIASFVRGCGASGLYPDAFAPVQFVNWIDSIIOR 219

Db 210 GLIHGIASFVRGCGASGLYPDAFAPVQFVNWIDSIIOR 248

#### RESULT 2

I48679  
neutrophil elastase - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
A;Accession: I48679  
R;Nuchprayoon, I.; Meyers, S.; Scott, L.M.; Suzow, J.; Hiebert, S.; Friedman, A.D.  
Mol. Cell. Biol. 14, 5558-5568, 1994  
A;Title: PEBP2/CBF, the murine homolog of the human myeloid AML1 and PEBP2 beta/CBF bet  
1s.  
A;Reference number: I48679; MUID:94305676; PMID:8035830  
A;Accession: I48679  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-265 <RES>  
A;Cross-references: UNIPROT:Q61515; EMBL:U04962; NID:9452556; PIDN:AAB60670.1; PID:9452  
C;Genetics:  
A;Introns: 22/1; 74/2; 121/3; 199/3  
C;Superfamily: trypsin; trypsin homology  
F;29-242/Domain: trypsin homology <TRY>

Query Match 76.2%; Score 868.5; DB 2; Length 265;  
Best Local Similarity 75.9%; Pred. No. 1.4e-72;  
Matches 167; Conservative 19; Mismatches 33; Indels 1; Gaps 1;

QY 1 IVGGRARPHAWPFMSQLQRGHFCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 60  
DB 29 IVGGRARPHAWPFMSQLQRGHFCGATLIAPNFVMSAAHCVANVAVRVVVLGAHNL 88  
QY 61 SRREPTQFAVQRIEFGNDPNNLLNDIVILQNGSATINAVQVLAQRRLLNGV 120  
DB 89 SRREPTQFAVQRIEFGNDPNNLLNDIVILQNGSATINAVQVLAQRRLLNGV 148  
QY 121 QCLAMGWLGRNRIASVQLQELNVTVTSLSLRSSNVCTLVGRQAGVCFGDSGPLVC 179  
DB 149 QCLAMGWLGRNRIASVQLQELNVTVTSLSLRSSNVCTLVGRQAGVCFGDSGPLVC 208  
QY 180 NGLIHGIASFVRGCGASGLYPDAFAPVQFVNWIDSIIOR 219  
DB 209 NNLVQGITDSFIRGCGSGLYPDAFAPVGEFVDWINSIIR 248

RESULT 3  
PRH03  
protease 3 (EC 3.4.21.-) precursor [validated] - human  
N;Alternate names: AGP7; C-ANCA antigen; neutrophil proteinase 4; p29; Wegener's granul  
N;Contains: myeloblastin  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
A;Accession: A45080; B42668; A43983; JH0331; A33751; S11091; A61176; A60148; A43982; A4;  
R;Sturrock, A.B.; Franklin, K.F.; Rao, G.; Marshall, B.C.; Rebentisch, M.B.; Lemons, R.;  
J. Biol. Chem. 267, 21193-21199, 1992  
A;Title: Structure, chromosomal assignment, and expression of the gene for proteinase-3  
A;Reference number: A45080; MUID:93016043; PMID:1400430  
A;Accession: A45080  
A;Molecule type: DNA  
A;Residues: 1-254, P, <STU>  
A;Cross-references: UNIPROT:P24158; GB:M97911  
A;Note: sequence extracted from NCBI backbone (NCBIP:116205)  
R;Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992  
A;Title: Three human elastase-like genes coordinately expressed in the myelomonocyte lin  
A;Reference number: A46268; MUID:92390417; PMID:1518849  
A;Accession: A46268  
A;Molecule type: DNA  
A;Residues: 1-118, V, 120-134, AT, 137-256 <ZTM>  
A;Note: sequence extracted from NCBI backbone (NCBIN:112898, NCBIN:112900, NCBIN:112902,  
R;Labbaye, C.; Musette, P.; Cayre, Y.E.  
Proc. Natl. Acad. Sci. U.S.A. 88, 9253-9256, 1991  
A;Title: Wegener autoantigen and myeloblastin are encoded by a single mRNA.

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OM protein - protein search, using sw model

Run on: April 18, 2005, 12:40:23 ; Search time 43 Seconds  
(without alignments)  
380.189 Million cell updates/sec

Title: US-10-733-288A-4

Perfect score: 1140

Sequence: 1 IVGGRRARPHAWFMVSLQ.....PDFAFVAQFVNWDSIIQR 219

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000 ,

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/prodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pcp.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	99.4	238	3	US-08-944-483-31
2	1133	99.4	238	6	Sequence 31, Appl Patent No. 5180819
3	1133	99.4	238	6	Sequence 46, Appl Patent No. 5180819
4	1133	99.4	267	2	Sequence 27, Appl Patent No. 5180819
5	791	69.4	271	3	Sequence 25, Appl Patent No. 5180819
6	639.5	56.1	229	4	Sequence 23, Appl Patent No. 5180819
7	639.5	56.1	231	4	Sequence 20, Appl Patent No. 5180819
8	639.5	56.1	256	4	Sequence 20, Appl Patent No. 5180819
9	639.5	56.1	256	4	Sequence 20, Appl Patent No. 5180819
10	638.5	56.0	229	2	Sequence 20, Appl Patent No. 5180819
11	638.5	56.0	229	4	Sequence 20, Appl Patent No. 5180819
12	638.5	56.0	229	4	Sequence 20, Appl Patent No. 5180819
13	638.5	56.0	229	5	Sequence 20, Appl Patent No. 5180819
14	638.5	56.0	229	3	Sequence 20, Appl Patent No. 5180819
15	632.5	55.5	229	3	Sequence 30, Appl Patent No. 5180819
16	632.5	55.5	256	4	Sequence 30, Appl Patent No. 5180819
17	581	51.0	214	6	Sequence 6271, Appl Patent No. 5180819
18	581	51.0	214	6	Sequence 6271, Appl Patent No. 5180819
19	572.5	50.2	215	6	Sequence 18, Appl Patent No. 5180819
20	572.5	50.2	215	6	Sequence 18, Appl Patent No. 5180819
21	485	42.5	222	2	Sequence 9, Appl Patent No. 5180819
22	480	42.1	222	1	Sequence 9, Appl Patent No. 5180819
23	480	42.1	222	1	Sequence 9, Appl Patent No. 5180819
24	480	42.1	225	3	Sequence 32, Appl Patent No. 5180819
25	480	42.1	251	4	Sequence 6112, Appl Patent No. 5180819
26	480	42.1	255	4	Sequence 9690, Appl Patent No. 5180819
27	477	41.8	221	2	Sequence 1, Appl Patent No. 5180819

28 424 37.2 219 2 US-08-925-708-2 Sequence 2, Appl  
29 377 33.1 240 1 US-08-278-091-11 Sequence 11, Appl  
30 377 33.1 240 1 US-08-483-859-11 Sequence 11, Appl  
31 377 33.1 240 1 US-08-472-173-11 Sequence 11, Appl  
32 377 33.1 240 2 US-08-487-167-11 Sequence 11, Appl  
33 377 33.1 240 2 US-08-482-816-11 Sequence 11, Appl  
34 377 33.1 240 2 US-08-296-149-11 Sequence 11, Appl  
35 377 33.1 240 2 US-08-801-499-11 Sequence 11, Appl  
36 377 33.1 240 2 US-08-615-271-11 Sequence 11, Appl  
37 377 33.1 240 3 US-09-074-660-11 Sequence 11, Appl  
38 377 33.1 240 3 US-09-074-659-11 Sequence 11, Appl  
39 377 33.1 240 3 US-09-106-468-11 Sequence 11, Appl  
40 377 33.1 240 3 US-09-106-466A-11 Sequence 11, Appl  
41 377 33.1 240 3 US-09-106-467-11 Sequence 11, Appl  
42 372 32.6 283 4 US-09-244-111-2 Sequence 2, Appl  
43 364 31.9 133 4 US-09-949-016-7471 Sequence 7471, Ap  
44 343.5 30.1 234 3 US-08-944-483-46 Sequence 46, Appl  
45 343.5 30.1 268 4 US-09-949-016-10712 Sequence 10712, A

#### ALIGNMENTS

#### RESULT 1

US-08-944-483-31  
; Sequence 31, Application US/08944483  
; Patent No. 6232456  
; GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6183.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 238 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

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; MOLECULE TYPE: No. 6232456e
; US-08-944-483-31

Query Match      99.4%; Score 1133; DB 3; Length 238;
Best Local Similarity 99.5%; Pred. No. 2.9e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
Db 1 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60

Qy 61 SRREPTQVFAVORIIFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120
Db 61 SRREPTQVFAVORIIFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120

Qy 121 QCLAMGGLGRNRGIASVLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVCN 180
Db 121 QCLAMGGLGRNRGIASVLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVCN 180

Qy 181 GLIHGIASFVRGGCAGSLYDPAFAPVAQFVNWIDSIQR 219
Db 181 GLIHGIASFVRGGCAGSLYDPAFAPVAQFVNWIDSIQR 219

RESULT 4
US-08-978-404B-46
; Sequence 46, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5968782e
US-08-978-404B-46

Query Match      99.4%; Score 1133; DB 2; Length 267;
Best Local Similarity 99.5%; Pred. No. 3.4e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
Db 30 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 89
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; MOLECULE TYPE: No. 6232456e
; US-08-944-483-31

Query Match      99.4%; Score 1133; DB 3; Length 238;
Best Local Similarity 99.5%; Pred. No. 2.9e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
Db 1 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60

Qy 61 SRREPTQVFAVORIIFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120
Db 61 SRREPTQVFAVORIIFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120

Qy 121 QCLAMGGLGRNRGIASVLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVCN 180
Db 121 QCLAMGGLGRNRGIASVLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVCN 180

Qy 181 GLIHGIASFVRGGCAGSLYDPAFAPVAQFVNWIDSIQR 219
Db 181 GLIHGIASFVRGGCAGSLYDPAFAPVAQFVNWIDSIQR 219

RESULT 2
5180819-4
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO: 4:
; LENGTH: 238
5180819-4

Query Match      99.4%; Score 1133; DB 6; Length 238;
Best Local Similarity 99.5%; Pred. No. 2.9e-118;
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60
Db 1 IVGRRARPHAMPFVMSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNL 60

Qy 61 SRREPTQVFAVORIIFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120
Db 61 SRREPTQVFAVORIIFENGTDPNLLNDIVILQNGSATINANVQVQLPAQGRRLGNGV 120

Qy 121 QCLAMGGLGRNRGIASVLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVCN 180
Db 121 QCLAMGGLGRNRGIASVLQELNVTVVTSLCRRSNVCTLVGRQAGVCFDGSGLVCN 180

Qy 181 GLIHGIASFVRGGCAGSLYDPAFAPVAQFVNWIDSIQR 219
Db 181 GLIHGIASFVRGGCAGSLYDPAFAPVAQFVNWIDSIQR 219

RESULT 3
5180819-4
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO: 4:
; LENGTH: 238
5180819-4
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Perez, Carl  
TITLE OF INVENTION: Compositions for the Inhibition of  
Protein Hormone Formation and Uses Thereof  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy  
STREET: 500 West Madison - 34th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60661  
COMPUTER READABLE FORM:

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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATI ON NUMBER: US/08/395,456C
FILING DATE: 28-Feb-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 0820.006/1296 11850US06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/775-8000
TELEFAX: 312/775-8100
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-08-395-456C-27

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Best Local Similarity 54.5%; Pred. NO. 3.4e-63;  
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps

Qy	1	IVGRRARPHAWPFMVSLQLR--GGHFCGATLIAPNFVMSAAHCVANVNVRAVRV	
Db	1	IVGHEAPHSRPPYMASLQMRGNPQSHFCGGTIIHPSFVLTAHCLURDIPQLRLNVVV	
Qy	58	HNLSRREPTRQVFAVQRIEFENGTDVPVNLNDIVILQLNGSATINANVQVLAQLPAQGR	
Db	61	HNVRTQETPQQHFSVAQVFLNNDYDAENKLNLDILLQLSSPANLSASVATVQLPQQDQ	
Qy	118	NGVQCLAMWGKLLGRNVRGIASVLQELNVTVTSLCRRSNVCTLVGRQAGVCFGDSG	
Db	121	HGTQCLAMGWRVGAHDPPAQLVQLQELNVTVTFFCRPHNICITFVPRRKAGICFGDSGA	
Qy	178	VCNGLLHGITASVVRGCCASGLYPDAFAPVAQFVNWIDSIIQR	219
Db	181	ICDGIITQIGDSFVWGCAFLPDPDFETRVALYVDWIRSLRR	222

RESULT 7  
US-08-395-456C-25  
; Sequence 25; Application US/08395456C  
Patent No. 6586222

AFFILIATION: HARELBECK, ROBERT E.  
 JEWELL, DAVID A.  
 KOTHS, KIRSTON E.  
 KRIEGLER, MICHAEL  
 PEREZ, CARL  
 TITLE OF INVENTION: COMPOSITIONS FOR THE INHIBITION OF  
 PROTEIN HORMONE FORMATION AND USES THEREOF  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MCANDREWS, HELD & MALLOY



us-10-733-288a-4-rai

Mon Apr 18 13:05:49 2005

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;
; STREET: 500 West Madison - 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,456C
; FILING DATE: 28-Feb-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 0820.006/1296 11850US06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/775-8100
; TELEFAX: 312/775-8100
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
;
; US-08-395-456C-23
;
; Query Match 56.1%; Score 639.5; DB 4; Length 231;
; Best Local Similarity 54.5%; Pred. No. 3.5e-63;
; Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;
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; QY 1 IVGGRRARHPWPMVSLQLR---GGHFCGATLIAPNFVMSAAHCVANVNAVVRVVLGA 57
; DB 3 IVGGHEAQPHSRPYMASLQMGNGFSGHFCGGTLIHPSEVLTAHCLRDIPQRLVNVVLGA 62
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; QY 58 HNLRSRETRQVAVORIFENGTPVNLNDIVILQNGSATINANVOVAQLPAQGRRLG 117
; DB 63 HNVRTQETQOHFSVAQVFLNNYDAENKNDILLIQLSSPANLSASVATVQLPQODQPPV 122
;
; QY 118 NGVQCLAMGWLGNRGIAVLQELNVTVTSLCRSNVCTLVGRQAGVCFGDSGSP 177
; DB 123 HGTQCLAMGWRGVGHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSG 182
;
; QY 178 VCNGLIHGIASVVRGGCAGSLYPAPAFVAFVFNWIDSIOR 219
; DB 183 ICDGIIQIGDSFVINGCATRFLFPDPFFTRVALYVDWIRSTLRR 224
;
; RESULT 8
; US-08-395-456C-23
; Sequence 23, Application US/08395456C
; Patent No. 6586222
;
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; Jowell, David A.
; Koths, Kirston E.
; Kriegler, Michael
; Perez, Carl
;
; TITLE OF INVENTION: Compositions for the Inhibition of
; Protein Hormone Formation and Uses Thereof
;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy
; STREET: 500 West Madison - 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,456C
; FILING DATE: 28-Feb-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 0820.006/1296 11850US06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/775-8100
; TELEFAX: 312/775-8100
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
;
; US-08-395-456C-23
;
; Query Match 56.1%; Score 639.5; DB 4; Length 256;
; Best Local Similarity 54.5%; Pred. No. 4e-63;
; Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;
;
; QY 1 IVGGRRARHPWPMVSLQLR---GGHFCGATLIAPNFVMSAAHCVANVNAVVRVVLGA 57
; DB 28 IVGGHEAQPHSRPYMASLQMGNGFSGHFCGGTLIHPSEVLTAHCLRDIPQRLVNVVLGA 87
;
; QY 58 HNLRSRETRQVAVORIFENGTPVNLNDIVILQNGSATINANVOVAQLPAQGRRLG 117
; DB 88 HNVRTQETQOHFSVAQVFLNNYDAENKNDILLIQLSSPANLSASVATVQLPQODQPPV 147
;
; QY 118 NGVQCLAMGWLGNRGIAVLQELNVTVTSLCRSNVCTLVGRQAGVCFGDSGSP 177
; DB 148 HGTQCLAMGWRGVGHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSG 207
;
; QY 178 VCNGLIHGIASVVRGGCAGSLYPAPAFVAFVFNWIDSIOR 219
; DB 208 ICDGIIQIGDSFVINGCATRFLFPDPFFTRVALYVDWIRSTLRR 249
;
; RESULT 9
; US-08-487-453A-23
; Sequence 23, Application US/08487453A
; Patent No. 6599706
;
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; Jowell, David A.
; Koths, Kirston E.
; Kriegler, Michael
; Perez, Carl
;
; TITLE OF INVENTION: Recombinant PR-3 and Assays Employing the Same
;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,453A
; FILING DATE:

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; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-394-600B-20

Query Match          56.0%; Score 638.5; DB 2; Length 229;
Best Local Similarity 54.1%; Pred. No. 4.4e-63;
Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

QY 1 IVGRRARPHAMPFMVSQLR---GGHFCGATLIAPNFVMSAAHCVANVNRVAVLGA 57
DB 1 IVGHEAQPHSRPYMASLQWRGNPGSHFCGGLIHPSEVLTAACHLRDIPQRLVNVVLGA 60
QY 58 HNLRRPEPTQVPAVORIEFENGTDTPVNLINDVILQNGSATNNANVQVAQLPAQGRRLG 117
DB 61 HNVRTQPTQHFSAQVFLNNYDAENKLNLDVLLQLSSPANLSASVATVQLPQQDQVP 120
QY 118 NGVOCLAMGGLLGRNKGASVLQELNVTVTSLCRRSNVCTLVGRQAGVCGDGSGL 177
DB 121 HGTQCLAMGWRGVAGDDPPAQVLQELNVTVTFPCPHNICTVPRKAGICFGDSGGL 180
QY 178 VCNGLIHGIASVRRGCASGLYDFAFAPVAQFVNWIDSIQR 219
DB 181 ICDGIIGQDSFVINGCATLFPDFPTRVALYVDWIRSTLR 222

RESULT 11
US-08-395-456C-20
; Sequence 20, Application US/08395456C
; Patent No. 6586222
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; Jewell, David A.
; Kotha, Kirston E.
; Kriegler, Michael
; Perez Carl
; TITLE OF INVENTION: Compositions for the Inhibition of
; Protein Hormone Formation and Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy
; STREET: 500 West Madison - 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,456C
; FILING DATE: 28-Feb-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 0820.006/1296 11850US06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/775-8000
; TELEFAX: 312/775-8100
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-395-456C-20

Query Match          56.0%; Score 638.5; DB 4; Length 229;
Best Local Similarity 54.1%; Pred. No. 4.4e-63;
Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 17a

Qy      1  IVGRRRAPHAPFNVSVLQLR--GGHFCGATLAPNFVMSAAHCVANVNVRAVRVLGA 57
Db      1  IVGGEAPHSRPNYMASIQMRGNPFGSHFCGGTLHPFSVLTAAHCLURDIPQRLNVNVLGA 60

Qy      58  HNLSRREPTRQVFAYORIFENGTPPVNLLNDIVLQNGSATINANVQVQLPFAQGRRIG 117
Db      61  HNVRQTEPTQQHFSVAQVFLNNDYDAENKINDVLLIQLSSPANLSASVATVQLPQQDQPPV 120

Qy      118  NGVQCLAMGWGLLGRNRIASVLOELNVTVVTSLCRRSNVCTIVRGQAGVCPGDSGSLP 177
Db      121  HGTQCLAMGWGRVGAHDPPAQVLOELNVTVVTFRCRPHNICTFVPRKAGICFGDSGSLP 180

Qy      178  VCNGLIHGTASVRRGCASGLYPDAFAVQVNWIDSLIQR 219
Db      181  ICDGIIQTGIDSFVINGCATRLFPDFTFVALYVDMWIRSTLRR 222

```

RESULT 12  
US-08-487-453A-20  
; Sequence 20, Application US/08487453A  
; Patent No. 6599706  
; GENERAL INFORMATION:  
; APPLICANT: Halenbeck, Robert F.  
; APPLICANT: Jewell, David A.  
; APPLICANT: Koths, Kirston E.  
; APPLICANT: Kriegler, Michael  
; APPLICANT: Perez, Carl  
; TITLE OF INVENTION: Recombinant PR-3 and Assays Employing the Same  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,453A

```

/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pochopien, Donald J.
/ REGISTRATION NUMBER: 32,167
/ REFERENCE/DOCKET NUMBER: 27527/32753
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 229 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-487-453A-20

```

```

QY 1 IVGGRARHPMPVYSLQLR--GGHFCGATLIAFNFMVMSAAHCVANVNVRAVRVVLGA 57
Db 1 IVGHEAQPHSRPVMASLQWGNPGSHFGCGTLLHPSFVLTAACHLRDIPQRLVNVVLGA 60
QY 58 HNLSREPTRQVFAVQRIEFENGTPDYNLNDIVYLOINGSATINANVQVAQLPAQGRRLG 117
Db 61 HNVRTQPTQQHESVAQVFLNNYDAENKLNVDVLLIQLSSPANLSASVATVQLPQDQPPV 120
QY 118 NGVQCLAMGWLGRNRGTASVLQELNVTVVTSLCRRSNVCTLVVRGQAGVCFDGSGL 177
Db 121 HGTQCLAMGWRGVRGHDPPAQVQLQELNVTVVTFPCRPHNICTFVPRKAGICFGDSGGL 180
QY 178 VCNGLHGTASVVRGGCAGLYPDADFAPVAQVFNWIDSIIOR 219
Db 181 ICDGIIGIDSFVWGCATLFPDFTPRVALYVDWIRSTLRR 222

RESULT 13
PCT-US95-02513-20
; Sequence 20, Application PC/TUS9502513
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; APPLICANT: Jewell, David A.
; APPLICANT: Koths, Kirston E.
; APPLICANT: Kriegler, Michael
; APPLICANT: Perez, Carl
; TITLE OF INVENTION: Compositions for the Inhibition of
; TITLE OF INVENTION: Protein Hormone Formation and Uses Thereof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02513
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27527/32404
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-02513-20

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	Query Match	56.0%	Score 638.5	DB 5	Length 229
	Best Local Similarity	54.1%	Pred. No. 4.4e-63		
	Matches 120	Conservative 41	Mismatches 58	Indels 3	Gaps 1
QY	1	IVGGRRARPHAMPFVMSLQLR	--GHGPCGATLAPNFVMSAHCVANVAVRVVLGA	57	
Db	1	IVGGHEAPHSRPFYMASIQMRNPGSHFCGGTLHP	SFVLTAACHLKKDIPQLRVNVVLGA	60	
QY	58	HNLSRREPTQVFAVQRI	FENGTPQVNLINDIVILQNGSATINNAVQVAQLPAQGRRLG	117	
nb	61	HNVRTOETPOOHFSVAQVFLNNYDAENKINDVLIQLSSPANLGS	VATVQPOODQVPP	120	

	Query Match	56.0%;	Score 638.5;	DB 2;	Length 256;	
	Best Local Similarity	54.1%;	Pred. No. 5.2e-63;			
	Matches 120;	Conservative 41;	Mismatches 58;	Indels 3;	Gaps 1;	
Qy	1	IVGRRARPHAMPFVMSLQLR---	GGHFCGATLIAPNFVMSAAHCVANVNVRAVRVLGA	57		
		:    :    :    :    :    :    :    :				
Db	28	IVGHEAQPHSRPYMASLQMRGNPGSHFCGGTIIHFSFVLTAACHLDRIPQLRVNVVLGA	87			
		:    :    :    :    :    :    :    :				
Qy	58	HNLRSRETRQVFAVORIFENGTDIPVNLNDIIVILQNGSATINANVQAQLPAQGRRLG	117			
		:    :    :    :    :    :    :    :				
Db	88	HNVRTQETQOHFSVAQVFLNNYDAENKLVLLIQLSPANLSASVATVQLPQDQVPV	147			
		:    :    :    :    :    :    :    :				
Qy	118	NGVQCILAMGWLIGLRNRGATSLVQLQELNNVTVTSLCRRSNVCTLVRGROAGVCFGDSGSLP	177			



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 12:27:28 ; Search time 174 Seconds  
(without alignments)  
486.785 Million cell updates/sec

Title: US-10-733-288A-4  
Perfect score: 1140  
Sequence: 1 IVGGRRAPHAQFWVSLQL.....PDAFAPVAQFVNWIDSIIR 219

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	99.4	238	7 ADJ68391	Adj68391 Human hea
2	1133	99.4	247	4 AAB55525	AAB55525 Human ela
3	1133	99.4	267	1 AAP80335	AAP80335 Sequence
4	1133	99.4	267	2 AAW64262	AAW64262 Human neu
5	1133	99.4	267	8 ADK42607	ADK42607 Human neu
6	1133	98.5	218	7 ADJ68281	Adj68281 Human hea
7	1114	97.7	218	5 AAU75897	AAU75897 Human leu
8	1064	93.3	257	5 ABP69417	ABP69417 Human pol
9	875.5	76.8	265	2 AAW70534	AAW70534 Mouse neu
10	872.5	76.5	265	2 AAR08269	AAR08269 Mouse ser
11	639.5	56.1	256	2 AAR85639	AAR85639 NY17 prep
12	639.5	56.1	256	7 ABW02656	ABW02656 Human mat
13	638.5	56.0	229	7 ABW02654	ABW02654 Human mat
14	638.5	56.0	256	2 AAR45403	AAR45403 Deduced s
15	638.5	56.0	256	7 ABW02646	ABW02646 Human pre
16	637.5	55.9	229	8 ADM67204	ADM67204 Human hom
17	637.5	55.9	229	7 ABW02679	ABW02679 Human mat
18	635.5	55.7	229	7 ABW02678	ABW02678 Human mat
19	635.5	55.7	253	8 ADM67203	ADM67203 Murine ad
20	634.5	55.7	229	7 ABW02676	ABW02676 Human mat
21	633.5	55.6	229	7 ABW02677	ABW02677 Human mat
22	632.5	55.5	229	7 ABW02680	ABW02680 Human mat
23	632.5	55.5	237	2 AAR20509	AAR20509 Human pro
24	632.5	55.5	256	5 ABB6770	ABB6770 Human pro
25	632.5	55.5	256	8 ADQ14416	ADQ14416 Human mye

26	632.5	55.5	256	8	ADR41702	ADR41702 Wegener's
27	569.5	50.0	215	2	AAR13036	AAR13036 Myeloblas
28	485.5	42.6	255	8	ADI16330	ADI16330 Human pro
29	485	42.5	222	2	AAW73210	AAW73210 CAP37 pro
30	483	42.4	225	7	ADE11551	ADE11551 Human mat
31	481	42.2	225	3	AAV71881	AAV71881 Human hep
32	480	42.1	222	2	AAV41935	AAV41935 Recombina
33	480	42.1	222	7	ADG42088	ADG42088 Human pol
34	480	42.1	225	2	AAW88362	AAW88362 Human mat
35	480	42.1	225	2	AAV21551	AAV21551 Human hep
36	480	42.1	225	2	AAW88118	AAW88118 Mature hu
37	480	42.1	225	3	AAV71883	AAV71883 Human hep
38	480	42.1	225	3	AAV71876	AAV71876 Human mat
39	480	42.1	225	4	AAV71891	AAV71891 Human mat
40	480	42.1	225	7	ADE11587	ADE11587 Human hep
41	480	42.1	225	8	ADK42019	ADK42019 Human hep
42	480	42.1	232	2	AAW88364	AAW88364 Human pro
43	480	42.1	232	2	AAV21550	AAV21550 Human hep
44	480	42.1	232	2	AAW88120	AAW88120 Human hep
45	480	42.1	232	3	AAV71877	AAV71877 Human pre

ALIGNMENTS

RESULT 1		
ADJ68391		
ID	ADJ68391 standard; protein; 238 AA.	
XX	ADJ68391;	
AC		
XX	06-MAY-2004 (first entry)	
DT		
XX		
DE	Human heat mitochondrial protein as a therapeutic target SegID197.	
XX		
KW	mitochondrial; human; screening assay; diabetes mellitus;	
KW	Huntington's disease; osteoarthritis;	
KW	Leber's hereditary optic neuropathy; LHON;	
KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;	
KW	myoclonic epilepsy tagged red fibre syndrome; MERRF; cancer;	
KW	neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;	
KW	osteopathic; ophthalmological; cytostatic.	
OS	Homo sapiens.	
XX		
PN	WO2003087768-A2.	
XX		
PD	23-OCT-2003.	
XX		
PF	04-APR-2003; 2003WO-US010870.	
XX		
PR	12-APR-2002; 2002US-0372843P.	
PR	17-JUN-2002; 2002US-0389987P.	
PR	20-SEP-2002; 2002US-0412418P.	
XX	(MITO-) MITOKOR.	
PA	(BUCK-) BUCK INST AGE RES.	
XX		
PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	
PI	Warnock DE;	
XX		
DR	WPI; 2003-845369/78.	
XX		
PT	Identifying a mitochondrial target for drug screening assays and for	
PT	treating diseases associated with altered mitochondrial function,	
PT	comprises detecting a modified polypeptide in a sample and correlating	
PT	with the disease.	
XX		
PS	Claim 1; SEQ ID NO 197; 180pp; English.	
XX		
CC	This invention relates to novel mitochondrial targets that can be used	
CC	for therapeutic intervention in treating a disease associated with	
CC	altered mitochondrial function. Specifically, it refers to a method for	

CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, neurotropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytotatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.

XX Sequence 238 AA;  
SQ  
Query Match 99.4%; Score 1133; DB 7; Length 238;  
Best Local Similarity 99.5%; Pred. No. 4.6e-68;  
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGGRRARPHAWPFVMSLQRLGGHFCGATLIAPNFVMSAAHCVANVRAVRVLGAHNL 60  
DB 1 IVGGRRARPHAWPFVMSLQRLGGHFCGATLIAPNFVMSAAHCVANVRAVRVLGAHNL 60  
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 120  
DB 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 120  
QY 121 QCLAMGWLLGRNRGIAASVLQELNVTVVTSLCRRSNVCTLVRRGQAGVCFDGSGLVNCN 180  
DB 121 QCLAMGWLLGRNRGIAASVLQELNVTVVTSLCRRSNVCTLVRRGQAGVCFDGSGLVNCN 180  
QY 181 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIQOR 219  
DB 181 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIQOR 219

RESULT 2  
AAB55525  
ID AAB55525 standard; protein; 247 AA.  
XX  
AC AAB55525;  
DT 07-MAR-2001 (first entry)  
DE Human elastase variant protein SEQ ID NO:95.  
KW Human; elastase; variant; substrate; mutant; mutagenesis; histidine;  
KW human neutrophil elastase; H43A; cytotatic; proteolysis; ADEPT;  
KW antibody-directed enzyme activated prodrug therapy.  
OS Homo sapiens.  
XX  
FN WO200068363-A2.  
XX  
PD 16-NOV-2000.  
XX  
PF 04-MAY-2000; 2000WO-US006692.  
XX  
PR 05-MAY-1999; 99US-0132640P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Carter PJ, Dall'acqua W, Rodrigues M;  
XX  
XX WPI; 2001-007389/01.  
DR N-PSDB; AAC8022.  
PT Elastase variant (H43A) having altered substrate specificity useful for  
PT antibody-directed enzyme activated prodrug therapy.  
XX  
XX Disclosure; Fig 2; 79pp; English.  
PS  
XX The present invention describes a purified elastase variant (I) with an

CC amino acid sequence different from that of a precursor elastase, the  
CC difference comprising a substitution of an active site histidine residue  
CC corresponding to residue 43 in human neutrophil elastase with a different  
CC amino acid residue so that (i) has substrate specificity substantially  
CC different from the precursor elastase. (i) has cytotatic activity, and  
CC can be used in antibody-directed enzyme activated prodrug therapy. The  
CC elastase variant can be used to cleave a particular substrate, especially  
CC those containing histidine residues at the substrate site. Site-specific  
CC proteolysis is useful in therapeutic applications, e.g. for antibody-  
CC directed enzyme activated prodrug therapy (ADEPT), AAC8022, AAC8023 and  
CC AAB55432 to AAB55526 represent sequences used in the exemplification of  
CC the present invention

XX Sequence 247 AA;  
SQ  
Query Match 99.4%; Score 1133; DB 4; Length 247;  
Best Local Similarity 99.5%; Pred. No. 4.8e-68;  
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGGRRARPHAWPFVMSLQRLGGHFCGATLIAPNFVMSAAHCVANVRAVRVLGAHNL 60  
DB 5 IVGGRRARPHAWPFVMSLQRLGGHFCGATLIAPNFVMSAAHCVANVRAVRVLGAHNL 64  
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 120  
DB 65 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVOVAQLPAQGRRLGNGV 124  
QY 121 QCLAMGWLLGRNRGIAASVLQELNVTVVTSLCRRSNVCTLVRRGQAGVCFDGSGLVNCN 180  
DB 125 QCLAMGWLLGRNRGIAASVLQELNVTVVTSLCRRSNVCTLVRRGQAGVCFDGSGLVNCN 184  
QY 181 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIQOR 219  
DB 185 GLIHGIASFVRGGCAGSLYDPDAFAPVAQFVNWIDSIQOR 223

RESULT 3  
AAP80335  
ID AAP80335 standard; protein; 267 AA.  
XX  
AC AAP80335;  
DT 25-MAR-2003 (revised)  
DT 04-OCT-1990 (first entry)  
DE Sequence of serine protease (SP) of human myeloid cell origin and leader  
DE peptide.  
XX Serine protease; myeloid cell; intravascular coagulation treatment;  
KW enzyme.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT Peptide 1..29  
FT Protein 30..267  
XX  
XX WO806621-A.  
XX  
XX 07-SEP-1988.  
XX  
XX 26-FEB-1988; 88WO-JP000205.  
XX  
XX 05-MAR-1987; 87JP-00050676.  
XX 09-SEP-1987; 87JP-00225540.  
XX  
XX (TORA ) TORAY IND INC.  
XX (AOKI/) AOKI Y.  
XX Aoki Y, Okano K, Naruto M, Shimizu H, Nakamura H;  
XX WPI; 1988-271161/38.  
DR N-PSDB; AAN80315.



XX Serine protease of human myeloid cell origin - useful in disseminated  
PT intravascular coagulation treatment.  
XX Disclosure; Fig 6; 52pp; Japanese.  
XX A SP of human myeloid cell origin is new. Also new are precursors of SP  
CC having an N-terminal splittable or signal peptide; DNA sequences coding  
CC for SPand precursors and transcription-controlling DNA sequence required  
CC for expression of the gene. SP has antithrombotic activity, useful in  
CC disseminated intravascular coagulation. By expression of protease gene in  
CC suitable transformat organism SP can be obtained in large quantity. SP  
CC DNA selected and cloned from a library of human myeloid cell origin,  
CC inserted in suitable vector and expressed in transformant by a suitable  
CC organism such as E.coli HMS-174 or HB-101 a yeast. (Updated on 25-MAR-  
CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)  
XX SQ Sequence 267 AA;

Query Match 99.4%; Score 1133; DB 1; Length 267;  
Best Local Similarity 99.5%; Pred. No. 5.1e-68;  
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 60  
DB 30 IVGRRARPHAPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 89  
QY 61 SRREPTQVFAVQRIFFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLNGV 120  
DB 90 SRREPTQVFAVQRIFFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLNGV 149  
QY 121 QCLAMGWLGRNRGIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 180  
DB 150 QCLAMGWLGRNRGIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 209  
QY 181 GLIHGTASFVRGGCAGSLYPDAFAPVAQFVNWIDSIIQR 219  
DB 210 GLIHGTASFVRGGCAGSLYPDAFAPVAQFVNWIDSIIQR 248

RESULT 4  
AAW64262  
ID AAW64262 standard; protein; 267 AA.  
XX AAW64262;  
AC AC  
XX 24-NOV-1998 (first entry)  
DT DT  
XX Human neutrophil elastase.  
DE MCP-7; mast cell protease 7; tryptase-7; serine protease; human;  
KW elastase; blood clot; anticoagulant; myocardial infarction; reocclusion;  
KW thromboembolism; cerebral embolism; thrombosis; therapy.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH Binding-site 55..68  
FT /note= "putative substrate binding site"  
FT  
XX WO9824886-A1.  
PN  
XX 11-JUN-1998.  
PD  
XX 25-NOV-1997; 97WO-US021620.  
PF  
XX 04-DEC-1996; 96US-0032354P.  
PR (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
XX Stevens RL;  
XX WPI; 1998-333308/29.  
DR

XX New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -  
PT are used to treat clot formation in e.g. myocardial infarction,  
XX reocclusion following angioplasty or pulmonary thrombo-embolism.  
XX Example; Page 78-79; 92pp; English.  
XX This polypeptide comprises the loop regions in the vicinity of the  
CC putative substrate binding site of human neutrophil elastase. The  
CC crystallographic structure of this region was used as a template  
CC structure to model the structure of the substrate-binding pocket of mouse  
CC mast cell protease 7 (mMCP-7, see AAW64233). The invention relates to  
CC mMCP-7 and related tryptase-7 proteases that can be used to prevent or  
CC inhibit fibrin clot formation. Such proteases can be used to treat  
CC disorders mediated by undesirable thrombus clot formation such as  
CC myocardial infarction and reocclusion following angioplasty of blood  
CC clots associated with pulmonary thromboembolism, deep vein thrombosis,  
CC cerebral embolism, renal vein and peripheral arterial thrombosis  
XX SQ Sequence 267 AA;

Query Match 99.4%; Score 1133; DB 2; Length 267;  
Best Local Similarity 99.5%; Pred. No. 5.1e-68;  
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGRRARPHAPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 60  
DB 30 IVGRRARPHAPFMVSLQLRGCGHFCGATLIAPNFVMSAAHCYANVNVRAVRVVLGAHNL 89  
QY 61 SRREPTQVFAVQRIFFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLNGV 120  
DB 90 SRREPTQVFAVQRIFFENGTDVNLNDIVILQNGSATINANVQVQLPAQGRRLNGV 149  
QY 121 QCLAMGWLGRNRGIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 180  
DB 150 QCLAMGWLGRNRGIASVQLQELNVTVTSLCRSSNVCTLVGRQAGVCFDGSGLVCN 209  
QY 181 GLIHGTASFVRGGCAGSLYPDAFAPVAQFVNWIDSIIQR 219  
DB 210 GLIHGTASFVRGGCAGSLYPDAFAPVAQFVNWIDSIIQR 248

RESULT 5  
ADK42607  
ID ADK42607 standard; protein; 267 AA.  
XX ADK42607;  
AC AC  
XX 20-MAY-2004 (first entry)  
DT DT  
XX Human neutrophil elastase.  
DE Human; heparin binding protein; HBP; neutrophil elastase; antibacterial;  
KW cytokine 11-6; monocyte; bacterial infection; sepsis; septic shock;  
KW disseminated intravascular coagulation; meningococcal meningitis;  
KW pneumococcal pneumonia; inflammatory response; cell apoptosis;  
KW suppressed immune system; cancer; autoimmune diseases; trauma.  
XX Homo sapiens.  
OS  
XX WO2004016653-A2.  
PN  
XX 26-FEB-2004.  
PD  
XX 14-AUG-2003; 2003WO-DK000542.  
PF  
XX 15-AUG-2002; 2002DK-00001212.  
PR 19-AUG-2002; 2002US-0404155P.  
PR 27-JUN-2003; 2003DK-00000987.  
XX (LEUK-) LEUKETOCH AS.  
XX Djurup R, Flogdaard HJ, Norris K;  
PI

XX WPI; 2004-257185/24.  
XX N-PSDB; ADK42607.  
XX New peptides of heparin-binding protein and/or human neutrophil elastase  
PT for manufacturing a medicament for the treatment of e.g. bacterial  
PT infections, disseminated intravascular coagulation, cancer or autoimmune  
PT diseases.  
XX  
XX Claim 52; SEQ ID NO 589; 211pp; English.  
XX  
XX The invention relates to an antibacterial peptide conforming to the  
CC generic peptide sequence appearing as ADK42632, the motif being derived  
CC from analysis of the protein sequences of human heparin binding protein,  
CC hBHP, pig pHP and human neutrophil elastase (hNLE). Also included are a  
CC process for producing the new peptide (comprising providing an expression  
CC vector containing a DNA sequence encoding one or more of the above-  
CC mentioned amino acid sequences, transforming host cells with the vector,  
CC culturing the transformed host cells and purifying the expressed peptide)  
CC and a pharmaceutical composition comprising the new peptide. The peptide  
CC is capable of inhibiting or stimulating the secretion of cytokine IL-6  
CC from monocytes. The peptides are useful in manufacturing a medicament for  
CC the treatment of Gram-negative or Gram-positive bacterial infection, such  
CC as sepsis, severe sepsis, septic shock, disseminated intravascular  
CC coagulation, meningococcal meningitis or pneumococcal pneumonia. These  
CC may also be used in manufacturing a medicament for the stimulation or  
CC inhibition of inflammatory response, for the prevention of cell  
CC apoptosis, or for the treatment of individuals having suppressed immune  
CC system, cancer, autoimmune diseases and/or trauma. The present sequence  
CC represents human neutrophil elastase.  
XX  
XX Sequence 267 AA;  
SQ  
Query Match 99.4%; Score 1133; DB 8; Length 267;  
Best Local Similarity 99.5%; Pred. No. 5.1e-68;  
Matches 218; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGRRARPHAWPFVMSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60  
DB 30 IVGRRARPHAWPFVMSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 89  
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVQLPAQRRLLNGV 120  
DB 90 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVQLPAQRRLLNGV 149  
QY 121 QCLANGWLLGNRGASVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGSPVLCN 180  
DB 150 QCLANGWLLGNRGASVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGSPVLCN 209  
QY 181 GLIHGIASFVRGGCASGLYPDAFAPVQFVNWIDSIIQR 219  
DB 210 GLIHGIASFVRGGCASGLYPDAFAPVQFVNWIDSIIQR 248  
RESULT 6  
ADJ68281  
ID ADJ68281 standard; protein; 218 AA.  
XX  
XX ADJ68281;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Human heat mitochondrial protein as a therapeutic target SeqID87.  
XX  
XX mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis; LHON;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX  
XX Homo sapiens.  
OS

XX PN WO2003087768-A2.  
XX PD 23-OCT-2003.  
XX  
XX 04-APR-2003; 2003WO-US010870.  
XX  
XX 12-APR-2002; 2002US-0372843P.  
XX PR 17-JUN-2002; 2002US-0389987P.  
XX PR 20-SEP-2002; 2002US-0412418P.  
XX  
XX (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX  
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;  
PI Warnock DE;  
XX  
XX WPI; 2003-845369/78.  
XX  
XX Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX  
XX Claim 1; SEQ ID NO 87; 180pp; English.  
XX  
XX This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nontropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
XX Sequence 218 AA;  
SQ  
Query Match 98.5%; Score 1123; DB 7; Length 218;  
Best Local Similarity 99.1%; Pred. No. 2e-67;  
Matches 216; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGRRARPHAWPFVMSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60  
DB 1 IVGRRARPHAWPFVMSLQLRGHCATLIAPNFVMSAAHCVANVAVRVVLGAHNL 60  
QY 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVQLPAQRRLLNGV 120  
DB 61 SRREPTQVFAVQRIFFENGTDVFNLLNDIVILQNGSATINANVQVQLPAQRRLLNGV 120  
QY 121 QCLANGWLLGNRGASVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGSPVLCN 180  
DB 121 QCLANGWLLGNRGASVQLQELNVVTSLCRRSNVCTLVGRQAGVCFGDSGSPVLCN 180  
QY 181 GLIHGIASFVRGGCASGLYPDAFAPVQFVNWIDSIIQ 218  
DB 181 GLIHGIASFVRGGCASGLYPDAFAPVQFVNWIDSIIQ 218  
RESULT 7  
AAU75897  
ID AAU75897 standard; peptide; 218 AA.  
XX  
XX AAU75897;  
XX  
XX 08-MAY-2002 (first entry)  
XX



QY	121	QCLAMGWLLGRNRGIASVLOELNVTVTSLCRRSNVCTLVNRGQAGVCFGDSGSLVCN	180
Db	150	QCLAMGWLLGRNRGIASVLOELNVTVTSLCRRSNVCTL-----GDSGSLVCN	199
QY	181	GLIHGIASFVRGGCAGSLYPDAFAPVAQFVNWIDSIIQR	219
Db	200	GLIHGIASFVRGGCAGSLYPDAFAPVAQFVNWIDSIIQR	238
RESULT 9			
AAW70534	ID	AAW70534 standard; protein; 265 AA.	
XX	AC	AAW70534;	
XX	DT	17-OCT-2003 (revised)	
DT	02-FEB-1999	(first entry)	
XX	DE	Mouse neutrophil elastase.	
XX	DE	Neutrophil elastase; mouse; transgenic animal; knockout animal;	
KW	KW	emphysema; cystic fibrosis; infection; animal model.	
XX	OS	Mus musculus; strain 129/SvJ.	
XX	FN	WO9844091-A1.	
XX	PD	08-OCT-1998.	
XX	PF	30-MAR-1998; 98WO-US006266.	
XX	PR	31-MAR-1997; 97US-0042871P.	
XX	PR	27-MAR-1998; 98US-00049279.	
XX	PA	(BARN-) BARNES-JEWISH HOSPITAL.	
XX	PI	Shapiro SD, Belaouaj A;	
XX	DR	WPI; 1998-557103/47.	
XX	DR	N-PSDB; AAV33754.	
XX	PT	New murine neutrophil elastase knockout transgenic mice - useful as	
XX	PT	models for studying disorders such as pulmonary emphysema.	
XX	PS	Claim 22; Page 45-46; 77pp; English.	
XX	CC	This is the amino acid sequence of murine neutrophil elastase (NE), as deduced from an open reading frame in an isolated cDNA clone (see AAV33754). NE has a specific role in host defence against Gram-positive but not Gram-negative bacteria. Vectors comprising NE nucleotide sequences, portions of these sequences, and transformed host cells harboring such vectors are also provided, as well as transgenic and knockout mice. Transgenic animals deficient in expression of NE can be used to study the physiological and pathological functions of NE and its interaction with other enzymes having a potential relationship to cardiopulmonary function and pathology, such as cystic fibrosis transmembrane conductance regulator. They can also be used as models for disorders such as pulmonary emphysema and for the role of NE in combating infection. NE-deficient animals can also be used as a source of cells for cell culture. (Updated on 17-OCT-2003 to standardise OS field)	
XX	SQ	Sequence 265 AA;	
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120
Query Match 76.8%; Score 875.5; DB 2; Length 265;			
Best Local Similarity 76.7%; Pred. No. 7.4e-51;			
Matches 168; Conservative 19; Mismatches 31; Indels 1; Gaps 1;			
QY	1	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	60
Db	29	IVGGRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNRVAVRVLGAHNL	88
QY	61	SRREPTQVFAVORIFENGTDPNVNLNDIVILQNGSATINANVOVAQLPAQGGRLNGV	120

QY 180 NGLIHGIASVRCGASGLYPDAFAPVAQFVNWIDSIIQ 218  
 Db 209 NNLVQIGDSPIRGCGSLYPDAFAPVABFADINSIIR 247

## RESULT 11

AAR85639  
 ID AAR85639 standard; protein; 256 AA.

XX AAR85639;  
 DT 23-APR-1996 (first entry)  
 XX MY17 preproPR-3.  
 KW PR-3; preproPR-3; MY17; human neutrophil protease-3; serine protease;  
 KW tumour necrosis factor alpha; TNFalpha; HL60; MY17; B cell; T cell;  
 KW tumour necrosis factor alpha convertase; cytokine; septic shock;  
 KW rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease;  
 KW ischaemia/reperfusion injury; autoimmune disease; AIDS.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..25 /note= "leader sequence present only in preproPR-3"  
 FT Peptide 26..27 /note= "dipeptide present in proPR-3"  
 FT Protein 28..256 /note= "mature PR-3"

XX WO9524501-A1.

XX 14-SRP-1995.

XX 02-MAR-1995; 95WO-US002513.

XX 07-MAR-1994; 94US-00208574.

PR 19-APR-1994; 94US-00230428.

PR 27-FEB-1995; 95US-00394600.

PR 28-FEB-1995; 95US-00395456.

XX (CETU ) CETUS ONCOLOGY CORP.

XX Halenbeck RF, Kriegler M, Perez C, Jewell DA, Koths KE;

XX N-PSDB; AAT02565.

XX Identification of inhibitors of mature TNFalpha prodn. - useful for

XX treatment of septic shock, rheumatoid arthritis, etc.

XX Example 2; Page 82; 96pp; English.

XX This sequence represents the preproPR-3. PR-3 is active recombinant human

XX neutrophil protease-3. PR-3 is a serine protease, and is a tumour

XX necrosis factor alpha (TNFalpha) convertase. The cDNA encoding this

XX sequence was isolated from the HL60 cell clone MY17. The mature PR-3 can

XX be used in the method of the invention for identifying agents that

XX inhibit cleavage of proTNFalpha to mature TNFalpha. In the method,

XX proTNFalpha is incubated with PR-3 (or another TNFalpha convertase), and

XX the cleavage of the proTNFalpha is measured by a colourimetric assay.

XX This is then repeated in the presence of a test compound that is thought

XX to inhibit this process. The results of the two reactions are then

XX compared to determine whether the test compound is an inhibitor. The

XX cleavage inhibitors can be used in the treatment of septic shock.

XX rheumatoid arthritis, cachexia, cerebral malaria, ischaemia/reperfusion

XX injury, graft-host disease, autoimmune diseases, and AIDS. PR-3 can be

XX used to treat unwanted B cell/T cell interaction by contacting it with T

XX cells to cause the release of membrane-bound cytokines

XX Sequence 256 AA;

Query Match 56.1%; Score 639.5; DB 2; Length 256;

Best Local Similarity 54.5%; Pred. No. 3.9e-35;

Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;

QY 1 IVGRRRAPHWPFVMSLQLR--GGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGA 57

Db 28 IVGGHEAQHSRPMASLQMRGNPGSHFCGGLIHPFVLTAAHCLRDIPQLRVNVVLGA 87

QY 58 HNLSRREPTQVAVQRIPEFNGCTDPVNLNDIVILQLNGSATINANVQVQLPAQGRRLG 117

Db 88 HNVRTQEPHQHFSVAQVELNNYDAENKLDILLQLSSPANLSASVATVQLPQQDQPPV 147

QY 118 NGVQCLAMGWLLGRNGIASVLQELNVTVTSLCRSNVCTLVRCRQAGVCEGDSGSL 177

Db 148 HGTQCLAMGWGRVGAHDPQAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDGGSL 207

QY 178 VCNGLIHGIASVRCGASGLYPDAFAPVAQFVNWIDSIIQ 219

Db 208 ICDGIIQIGDSPVWGCAITLFPDFTRVALYVDWIRSLRR 249

XX Human preproPR-3 protein from MY17 clone.

XX Human; tumour necrosis factor alpha; neutrophil protease; PR-3; P-29b;

XX serine protease; proteinase-3; myeloblastin; Wegener's granulomatosis;

XX rheumatoid arthritis; acquired immune deficiency syndrome; cachexia;

XX TNFalpha convertase; sepsis; therapy; autoimmune disease; AIDS; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..25 /note= "PR-3 leader peptide"

FT Peptide 26..27 /note= "proPR-3 peptide"

FT Protein 28..256 /note= "Human mature PR-3 protein"

XX US6599706-B1.

XX 29-JUL-2003.

XX 07-JUN-1995; 95US-00487453.

XX 16-AUG-1989; 89US-00395253.

PR 07-MAR-1994; 94US-00208574.

PR 14-APR-1994; 94US-00230428.

PR 27-FEB-1995; 95US-00394600.

PR 28-FEB-1995; 95US-00395456.

XX (CHIR ) CHIRON CORP.

XX Halenbeck RF, Kriegler M, Tuttleman J, Perez C, Jewell DA;

PI Koths KE;

XX WPI; 2003-851193/79.

DR N-PSDB; AAD64612.

XX Determination of presence of inhibitor human-neutrophil protease by,

XX contacting recombinant mature human-neutrophil protease having specified

XX sequence of amino acids, with sample having inhibitor of human-neutrophil

XX protease.

XX Claim 1; SEQ ID NO 23; Opp; English.

XX

CC The invention relates to TNFalpha (tumour necrosis factor alpha)  
CC convertase, a human-neutrophil protease (PR-3) capable of converting pro-  
CC TNFalpha to mature TNFalpha. PR-3 (serine protease) is also referred to  
CC as proteinase-3, P-29b and myeloblastin. The invention specifically  
CC relates to the identification of compositions and methods for identifying  
CC inhibitors of TNFalpha convertase. Inhibitors of the invention are used  
CC for determining Wegener's granulomatosis and for treating diseases  
CC associated with elevated levels of hormones particularly sepsis,  
CC rheumatoid arthritis, cachexia, acquired immune deficiency syndrome  
CC (AIDS) and autoimmune diseases. The present sequence is human preproPR-3  
CC protein  
XX  
SQ Sequence 256 AA;  
Query Match 56.1%; Score 639.5; DB 7; Length 256;  
Best Local Similarity 54.5%; Pred. No. 3.9e-35;  
Matches 121; Conservative 40; Mismatches 58; Indels 3; Gaps 1;  
QY 1 IVGRRARPHAMPFVMSLQLR---GGHFCGATLIAPNFVMSAAHCYANVNVRAVRVLGA 57  
DB 28 IVGGHEAQPSPRYMASLQMRGNPGSHFCGGTLIHPFVLTAACHLURDIPOQLNVNVVILGA 87  
QY 58 HNLSSRREPTROVFAVORIFENGTDVNLNDIVILQNGSATINANVQVAPQAGRRIG 117  
DB 88 HNVRTQEPHQHFSVAQVFLNNYDAENKLDNLIQLSSPANLSASVATVQLPQQDQVPV 147  
QY 118 NGVOCLAMGWLGLGRNGIASVLQELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPL 177  
DB 148 HGTQCLAMGWRVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 207  
QY 178 VCNGLIHGIASFVRGCGASGLYPDAFAPVAFVNWIDSIIOR 219  
DB 208 ICDGIIQIGDSFVIWGCATRLFPDFFTRVALYVDWIRSTLRR 249  
RESULT 13  
ABW02654  
ID ABW02654 standard; protein; 229 AA.  
AC ABW02654;  
XX  
XX 11-MAR-2004 (first entry)  
XX Human mature PR-3 protein.  
DE  
XX Human; tumour necrosis factor alpha; neutrophil protease; PR-3; P-29b;  
KW serine protease; proteinase-3; myeloblastin; Wegener's granulomatosis;  
KW rheumatoid arthritis; acquired immune deficiency syndrome; cachexia;  
KW TNFalpha convertase; sepsis; therapy; autoimmune disease; AIDS; enzyme.  
XX  
XX Homo sapiens.  
XX US6599706-B1.  
XX  
XX 29-JUL-2003.  
XX  
XX 07-JUN-1995; 95US-00487453.  
XX  
XX 16-AUG-1989; 89US-00395253.  
XX 07-MAR-1994; 94US-00208574.  
XX 14-APR-1994; 94US-00230428.  
XX 27-FEB-1995; 95US-00394600.  
XX 28-FEB-1995; 95US-00395456.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX Halenbeck RF, Kriegler M, Tuttleman J, Perez C, Jewell DA;  
PI Koths KE;  
XX  
XX WPI; 2003-851193/79.  
DR N-PSDB; AAD64602.  
XX  
XX Determination of presence of inhibitor human-neutrophil protease by,

PT contacting recombinant mature human-neutrophil protease having specified  
PT sequence of amino acids, with sample having inhibitor of human-neutrophil  
PT protease.  
XX  
XX Disclosure; SEQ ID NO 20; Opp; English.  
XX  
XX The invention relates to TNFalpha (tumour necrosis factor alpha)  
CC convertase, a human-neutrophil protease (PR-3) capable of converting pro-  
CC TNFalpha to mature TNFalpha. PR-3 (serine protease) is also referred to  
CC as proteinase-3, P-29b and myeloblastin. The invention specifically  
CC relates to the identification of compositions and methods for identifying  
CC inhibitors of TNFalpha convertase. Inhibitors of the invention are used  
CC for determining Wegener's granulomatosis and for treating diseases  
CC associated with elevated levels of hormones particularly sepsis,  
CC rheumatoid arthritis, cachexia, acquired immune deficiency syndrome  
CC (AIDS) and autoimmune diseases. The present sequence is human mature PR-3  
CC protein  
XX  
SQ Sequence 229 AA;  
Query Match 56.0%; Score 638.5; DB 7; Length 229;  
Best Local Similarity 54.1%; Pred. No. 4.1e-35;  
Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;  
QY 1 IVGRRARPHAMPFVMSLQLR---GGHFCGATLIAPNFVMSAAHCYANVNVRAVRVLGA 57  
DB 1 IVGGHEAQPSPRYMASLQMRGNPGSHFCGGTLIHPFVLTAACHLURDIPOQLNVNVVILGA 60  
QY 58 HNLSSRREPTROVFAVORIFENGTDVNLNDIVILQNGSATINANVQVAPQAGRRIG 117  
DB 61 HNVRTQEPHQHFSVAQVFLNNYDAENKLDNLIQLSSPANLSASVATVQLPQQDQVPV 120  
QY 118 NGVOCLAMGWLGLGRNGIASVLQELNVTVTSICRRSNVCTLVGRQAGVCFGDSGPL 177  
DB 121 HGTQCLAMGWRVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGPL 180  
QY 178 VCNGLIHGIASFVRGCGASGLYPDAFAPVAFVNWIDSIIOR 219  
DB 181 ICDGIIQIGDSFVIWGCATRLFPDFFTRVALYVDWIRSTLRR 222  
RESULT 14  
AAR45403  
ID AAR45403 standard; protein; 256 AA.  
XX  
XX AAR45403;  
XX AC  
XX 25-MAR-2003 (revised)  
DT 18-JUL-1994 (first entry)  
XX  
XX Deduced sequence of human proteinase-3 (PR-3).  
XX TNF convertase; proteinase-3; PR-3; tumour necrosis factor; proTNF.  
XX Homo sapiens.  
XX OS  
XX WO9400555-A2.  
XX  
XX 06-JAN-1994.  
XX  
XX 25-JUN-1993; 93WO-US006120.  
XX  
XX 25-JUN-1992; 92US-00905546.  
XX  
XX (CETU ) CETUS ONCOLOGY CORP.  
XX  
XX Kriegler M, Perez C, Halenbeck RF, Jewell DA, Koths KE;  
PI  
XX WPI; 1994-026195/03.  
DR N-PSDB; AAQ54498.  
XX  
XX Cpd. which inhibit formation of mature tumour necrosis factor from its  
PT precursor - identified using TNF convertase, e.g. mutein(s), antibodies

or peptide phosphate(s), for preventing and treating sepsis, AIDS, auto  
-immune disease etc.

Disclosure; Fig 2; 69pp; English.

ProTNF refers to TNF having a molecular weight of about 26,000, which is  
the prohormone form of TNF $\alpha$ . ProTNF is cleaved to a lower molecular  
weight 'mature' form, pref. 17kd, which, in its multimeric (usually  
trimeric) form, is substantially involved in producing life- threatening  
physiological changes associated with sepsis. ProTNF is cleaved by  
convertase. One TNF convertase is serine protease proteinase-3, also  
called PR-3. P-29B or myeloblastin. A suitable source of convertase is the  
HL60 cell line (or extracts, or the culture media in which it is grown).  
The convertase produced by HL60 has been sequenced and is identical to  
the known lymphocyte serine protease PR-3 which has other activities  
unrelated to TNF processing. (Updated on 25-MAR-2003 to correct PN  
field.)

Sequence 256 AA;

Query Match 56.0%; Score 638.5; DB 2; Length 256;  
Best Local Similarity 54.1%; Pred. No. 4.5e-35;  
Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;  
QY 1 IVGGRRARPHAWPFMVSLQLR---GGHFCGATLIAPNFVMSAAHCVANVAVRVVLGA 57  
DB 28 IVGGHEAQPHSRPYMASLQMRGNPGSHFCGGTLIHPSFVLTAACHLRDIPQLRVNVLGA 87  
QY 58 HNLSRREPTRQVAVORIPFENGTDVNLNDIVILQNGSATINANVQVAQLPAQGRRLG 117  
DB 88 HNVRTQEPHQHFSVAQVFLNNYDAENKLDVLLIQSSPANLSASVATVQLPQQQVP 147  
QY 118 NGVQCLAMGWLGRNRIASVQLQELNVTVTSLCRSNVCTLVRCQAGVCFDGSGL 177  
DB 148 HGTQCLAMGWGRVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGL 207  
QY 178 VCNGLTHGIASFVGGCAGSLYDPAPVAQVFNWIDSIQR 219  
DB 208 ICDGIIQIGDSFVINGCATRLFPDFTRVALYVDWIRSLRR 249

RESULT 15

ABW02646  
ID ABW02646 standard; protein; 256 AA.

AC ABW02646;

XX 11-MAR-2004 (first entry)

XX Human preproPR-3 protein.

XX Human; tumour necrosis factor alpha; neutrophil protease; PR-3; P-29b;  
KW serine protease; proteinase-3; myeloblastin; Wegener's granulomatosis;  
KW rheumatoid arthritis; acquired immune deficiency syndrome; cachexia;  
KW TNFalpha convertase; sepsis; therapy; autoimmune disease; AIDS; enzyme.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..25 "PR-3 leader peptide"

FT Peptide 26..27

FT Peptide /note= "proPR-3 peptide"

FT Protein 28..256

FT /note= "Human mature PR-3 protein"

XX US6599706-B1.

PN 29-JUL-2003.

XX 07-JUN-1995; 95US-00487453.

XX 16-AUG-1989; 89US-00395253.

PR 07-MAR-1994; 94US-00208574.  
PR 14-APR-1994; 94US-00230428.  
PR 27-FEB-1995; 95US-00394600.  
PR 28-FEB-1995; 95US-00395456.

XX (CHIR ) CHIRON CORP.

XX Halenbeck RP, Kriegler M, Tuttleman J, Perez C, Jewell DA;  
PI Koths KG;

XX WPI; 2003-851193/79.

XX N-PSDB; AAD64602.

Determination of presence of inhibitor human-neutrophil protease by,  
PT contacting recombinant mature human-neutrophil protease having specified  
PT sequence of amino acids, with sample having inhibitor of human-neutrophil  
PT protease.

XX Disclosure; Col 49-52; Opp; English.

XX The invention relates to TNFalpha (tumour necrosis factor alpha)  
CC convertase, a human-neutrophil protease (PR-3) capable of converting pro-  
CC TNFalpha to mature TNFalpha. PR-3 (serine protease) is also referred to  
CC as proteinase-3, P-29b and myeloblastin. The invention specifically  
CC relates to the identification of compositions and methods for identifying  
CC inhibitors of TNFalpha convertase. Inhibitors of the invention are used  
CC for determining Wegener's granulomatosis and for treating diseases  
CC associated with elevated levels of hormones particularly sepsis,  
CC rheumatoid arthritis, cachexia, acquired immune deficiency syndrome  
CC (AIDS) and autoimmune diseases. The present sequence is human preproPR-3  
CC protein

XX Sequence 256 AA;

Query Match 56.0%; Score 638.5; DB 7; Length 256;  
Best Local Similarity 54.1%; Pred. No. 4.5e-35;  
Matches 120; Conservative 41; Mismatches 58; Indels 3; Gaps 1;

QY 1 IVGGRRARPHAWPFMVSLQLR---GGHFCGATLIAPNFVMSAAHCVANVAVRVVLGA 57

DB 28 IVGGHEAQPHSRPYMASLQMRGNPGSHFCGGTLIHPSFVLTAACHLRDIPQLRVNVLGA 87

QY 58 HNLSRREPTRQVAVORIPFENGTDVNLNDIVILQNGSATINANVQVAQLPAQGRRLG 117

DB 88 HNVRTQEPHQHFSVAQVFLNNYDAENKLDVLLIQSSPANLSASVATVQLPQQQVP 147

QY 118 NGVQCLAMGWLGRNRIASVQLQELNVTVTSLCRSNVCTLVRCQAGVCFDGSGL 177

DB 148 HGTQCLAMGWGRVGAHDPPAQVQLQELNVTVTFFCRPHNICTFVPRKAGICFGDSGGL 207

QY 178 VCNGLTHGIASFVGGCAGSLYDPAPVAQVFNWIDSIQR 219

DB 208 ICDGIIQIGDSFVINGCATRLFPDFTRVALYVDWIRSLRR 249

Search completed: April 18, 2005, 12:46:20  
Job time : 176 secs

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